

GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: January 22, 2004, 12:55:27 ; Search time 50 Seconds

(without alignments)

2886.646 Million cell updates/sec

Title: US-09-541-462b-1

Perfect score: 327

Sequence: 1 atggcgagcagcgatggatgt.....tccaaaagtggcactag 327

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 569978 seqs, 220691566 residues

Total number of hits satisfying chosen parameters: 1139956

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents NA:\*

- 1: /cgn2\_6/prodata/1/ina/5A\_COMB.seq:\*
- 2: /cgn2\_6/prodata/1/ina/5B\_COMB.seq:\*
- 3: /cgn2\_6/prodata/1/ina/6A\_COMB.seq:\*
- 4: /cgn2\_6/prodata/1/ina/6B\_COMB.seq:\*
- 5: /cgn2\_6/prodata/1/ina/PCTUS\_COMB.seq:\*
- 6: /cgn2\_6/prodata/1/ina/backfiles1.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	253.6	77.6	3208	4	US-09-780-016-27
2	90	27.5	301	4	US-09-313-294A-492
3	31	9.5	2408	1	US-08-608-241-1
4	31	9.5	2408	2	US-08-922-182-1
5	31	9.5	2408	2	US-08-919-953-1
6	31	9.5	2408	3	US-09-192-983-1
7	30	9.2	648	4	US-09-599-360B-27
8	29.2	8.9	2951	1	US-08-386-727-7
9	29.2	8.9	2951	2	US-08-600-452A-7
10	28.6	8.7	648	4	US-09-252-991A-4236
11	28.6	8.7	723	4	US-09-252-991A-9470
12	28.6	8.7	1080	1	US-07-598-873-1
13	28.6	8.7	1080	1	US-08-073-425-1
14	28.6	8.7	1080	1	US-08-396-531-1
15	28.6	8.7	1488	4	US-09-252-991A-4168
16	28.6	8.7	2618	4	US-09-857-556A-25
17	28.4	8.7	3420	1	US-08-117-491-25
18	28.4	8.7	3420	1	US-08-271-364A-6
19	28.4	8.7	3420	2	US-08-222-715B-25
20	28.4	8.7	4707	1	US-08-004-139B-2
21	28.4	8.7	4707	2	US-08-811-492-2
22	28.4	8.7	4707	5	PCT-US96-10545A-2
23	28.4	8.7	35524	3	US-08-923-137-1
24	28.2	8.6	31880	4	US-09-453-702B-242
25	28	8.6	42931	4	US-08-311-731A-129
26	27.6	8.4	903	4	US-09-107-532A-2965
27	27.6	8.4	70000	4	US-09-851-896-3

28	27.4	8.4	261	4	US-08-651-155B-141	Sequence 141, App
29	27.4	8.4	261	4	US-09-194-036B-141	Sequence 141, App
30	27.4	8.4	1569	2	US-08-743-637B-176	Sequence 176, App
31	27.4	8.4	1569	3	US-08-526-840B-176	Sequence 176, App
32	27.4	8.4	4266	4	US-09-651-011A-3	Sequence 3, Appli
33	27.2	8.3	1131	2	US-08-758-621-9	Sequence 9, Appli
34	27.2	8.3	1131	3	US-09-107-858-9	Sequence 9, Appli
35	27.2	8.3	1134	4	US-09-252-991A-5445	Sequence 5445, Ap
36	27.2	8.3	1272	4	US-09-107-532A-1918	Sequence 1918, Ap
37	27.2	8.3	1437	4	US-09-252-991A-5507	Sequence 5507, Ap
38	27.2	8.3	1599	4	US-09-252-991A-5468	Sequence 5468, Ap
39	27.2	8.3	2436	4	US-09-252-991A-5435	Sequence 5435, Ap
40	27.2	8.3	2811	5	PCT-US94-05905-21	Sequence 21, Appli
41	27.2	8.3	2820	2	US-08-906-488-1	Sequence 1, Appli
42	27.2	8.3	2820	5	PCT-US94-05905-19	Sequence 19, Appli
43	27.2	8.3	4643	4	US-09-453-702B-22	Sequence 22, Appli
44	26.8	8.2	1551	4	US-09-252-991A-5309	Sequence 5309, Ap
45	26.8	8.2	1563	4	US-09-252-991A-15934	Sequence 15934, A

ALIGNMENTS

RESULT 1

US-09-780-016-27  
; Sequence 27, Application US/09780016  
; Patent No. 6509456  
; GENERAL INFORMATION:  
; APPLICANT: Donoho, Gregory  
; APPLICANT: Scoville, John  
; APPLICANT: Turner, C. Alexander Jr.  
; APPLICANT: Friedrich, Glenn  
; APPLICANT: Abuin, Alejandro  
; APPLICANT: Zambrowicz, Brian  
; APPLICANT: Sands, Arthur T.  
; TITLE OF INVENTION: No. 6509456el Human Proteases and  
; TITLE OF INVENTION: Polynucleotides Encoding the Same  
; FILE REFERENCE: LEX-0132-USA  
; CURRENT APPLICATION NUMBER: US/09/780,016  
; CURRENT FILING DATE: 2001-02-09  
; PRIOR APPLICATION NUMBER: US 60/181,294  
; PRIOR FILING DATE: 2000-02-11  
; NUMBER OF SEQ ID NOS: 27  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 27  
; LENGTH: 3208  
; TYPE: DNA  
; ORGANISM: homo sapiens  
US-09-780-016-27

Query Match	77.6%	Score 253.6;	DB 4;	Length 3208;
Best Local Similarity	98.5%	Pred No. 4.2e-78;		
Matches	256;	Conservative 0;	Mismatches 4;	Indels 0;
Gaps	0;			
QY	68	AAGTGAAGAAGTGGAAATGCAGTAGCCCTCTGGCCCTGGGATATGTGGTTGATAACTGTG	127	
DB	2765	AAAAAAAAAATGGAATGCAGTAGCCCTCTGGCCCTGGGATATGTGGTTGATAACTGTG	2824	
QY	128	CCATCTGCAGGAACACACATTATGGATCTTTGCATAGAAATGTCAAGCTAACACAGGCGTCCG	187	
DB	2825	CCATCTGCAGGAACACACATTATGGATCTTTGCATAGAAATGTCAAGCTAACACAGGCGTCCG	2884	
QY	188	CTACTTCAGACAGTGTACTGTGCGATGGGAGTCTGTAACCATGCTTTTCACTTCCACT	247	
DB	2885	CTACTTCAGACAGTGTACTGTGCGATGGGAGTCTGTAACCATGCTTTTCACTTCCACT	2944	
QY	248	GCATCTCTCGTGGCTCAAAACACACAGAGGTGTGTCATTGGACAAACAGAGTGGGAAT	307	
DB	2945	GCATCTCTCGTGGCTCAAAACACACAGAGGTGTGTCATTGGACAAACAGAGTGGGAAT	3004	
QY	308	TCCAAAGTATGGCACTAG	327	
DB	3005	TCCAAAGTATGGCACTAG	3024	





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Query Match          9.5%; Score 31; DB 3; Length 2408;
Best Local Similarity 53.8%; Pred. No. 1.1;
Matches 64; Conservative 0; Mismatches 55; Indels 0; Gaps 0;

QY 27 CCGGACGGCACCACAGCGCGCGGCGGCAAGAGCCCTTTGAAGTGAAGAAAGTGAATGC 86
DB 351 CACCCGTCGCGCGCTCGCCGTCGAGCGCGCAAGCGCTCGAGATCATGGAGGTCAATCT 410
QY 87 AGTAGCCCTCTGGGCTGGGATATTGTTGTTGATAACTGTGCCATCTGCAGGAACACCA 145
DB 411 CGAAGGCCCAAGCGCGGAGGTCTATGTCGAGATCAAGGCCACCGGATCTGCCACA 469

RESULT 7
US-09-599-3608-27
; Sequence 27, Application US/095993608
; Patent No. 6548633
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Bougueleret, L.
; APPLICANT: Jobert, S.
; TITLE OF INVENTION: Complementary DNA's Encoding Proteins with Signal Peptides
; FILE REFERENCE: GENSET:050CP3
; CURRENT APPLICATION NUMBER: US/09/599,3608
; CURRENT FILING DATE: 2000-06-21
; PRIOR APPLICATION NUMBER: 60/113,686
; PRIOR FILING DATE: 1998-12-22
; PRIOR APPLICATION NUMBER: 60/141,032
; PRIOR FILING DATE: 1999-06-25
; PRIOR APPLICATION NUMBER: 09/469,099
; PRIOR FILING DATE: 1999-12-21
; NUMBER OF SEQ ID NOS: 123
; SOFTWARE: Patent.pm
; SEQ ID NO 27
; LENGTH: 648
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 187..438
; NAME/KEY: polyA signal
; LOCATION: 612..617
; NAME/KEY: polyA site
; LOCATION: 632..648
US-09-599-3608-27

Query Match          9.2%; Score 30; DB 4; Length 648;
Best Local Similarity 57.4%; Pred. No. 1.3;
Matches 54; Conservative 0; Mismatches 40; Indels 0; Gaps 0;

QY 79 TGGAAATGCAGTAGCCCTCTGGGCTGGGATATTGTGTTGATAACTGTGCCATCTGCAGG 138
DB 208 TGGAAACGGGTGGCCACTTGCTCTGGTGGCCCAAGATGAGAACTGTGGCATCTGCAGG 267
QY 139 AACCAATATGATCTTTTGATAGAAATGTCAAG 172
DB 268 ATGGCATTAAACGGATGCTGCCCTGACTGCAAG 301

RESULT 8
US-08-386-727-7/c
; Sequence 7, Application US/08386727
; Patent No. 5792647
; GENERAL INFORMATION:
; APPLICANT: ROSEMAN, SAUL
; APPLICANT: BASSLER, BONNIE
; APPLICANT: KEYHANI, NEMAT O.
; APPLICANT: CHITLARU, EDITH
; APPLICANT: ROWE, CHRIS
; APPLICANT: YU, CHARLES
; TITLE OF INVENTION: BACTERIAL CATABOLISM OF CHITIN
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:

QY 27 CCGGACGGCACCACAGCGCGCGGCGGCAAGAGCCCTTTGAAGTGAAGAAAGTGAATGC 86
DB 351 CACCCGTCGCGCGCTCGCCGTCGAGCGCGCAAGCGCTCGAGATCATGGAGGTCAATCT 410
QY 87 AGTAGCCCTCTGGGCTGGGATATTGTTGTTGATAACTGTGCCATCTGCAGGAACACCA 145
DB 411 CGAAGGCCCAAGCGCGGAGGTCTATGTCGAGATCAAGGCCACCGGATCTGCCACA 469

RESULT 9
US-08-600-452A-7/c
; Sequence 7, Application US/08600452A
; Patent No. 5985644
; GENERAL INFORMATION:
; APPLICANT: ROSEMAN, SAUL
; APPLICANT: BASSLER, BONNIE
; APPLICANT: KEYHANI, NEMAT O.
; APPLICANT: CHITLARU, EDITH
; APPLICANT: ROWE, CHRIS
; APPLICANT: YU, CHARLES
; TITLE OF INVENTION: BACTERIAL CATABOLISM OF CHITIN
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FISH & RICHARDSON P.C.
; STREET: 4225 Executive Square, Suite 1400
; CITY: La Jolla
; STATE: CA
; COUNTRY: USA
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/600,452A
; FILING DATE: 13-FEB-1996
```

```
ADDRESSEE: CUSHMAN, DARBY & CUSHMAN
STREET: 1100 NEW YORK AVENUE, N.W.
CITY: WASHINGTON
STATE: D.C.
COUNTRY: USA
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/386,727
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: HOBBS, ANN S.
REGISTRATION NUMBER: 36,930
REFERENCE/DOCKET NUMBER: 4130/206916
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-861-3000
TELEFAX: 202-822-0944
TELEX: 6714627 CUSH
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 2951 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-386-727-7

Query Match          8.9%; Score 29.2; DB 1; Length 2951;
Best Local Similarity 62.2%; Pred. No. 5.3;
Matches 46; Conservative 0; Mismatches 28; Indels 0; Gaps 0;

QY 3 GCGCGCAGCGATGGATGGATACCCCGAGCGGCACCAACAGCGCGCGGCAAGGCG 62
DB 151 GCGCGCAGCGAGGCGGAGGTAGAACAGAGCCCCCGACCAATGCCAGGGAATG 92
QY 63 CTTTGAAGTGAATA 76
DB 91 TTTTGGACTGAACA 78

RESULT 9
US-08-600-452A-7/c
; Sequence 7, Application US/08600452A
; Patent No. 5985644
; GENERAL INFORMATION:
; APPLICANT: ROSEMAN, SAUL
; APPLICANT: BASSLER, BONNIE
; APPLICANT: KEYHANI, NEMAT O.
; APPLICANT: CHITLARU, EDITH
; APPLICANT: ROWE, CHRIS
; APPLICANT: YU, CHARLES
; TITLE OF INVENTION: BACTERIAL CATABOLISM OF CHITIN
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FISH & RICHARDSON P.C.
; STREET: 4225 Executive Square, Suite 1400
; CITY: La Jolla
; STATE: CA
; COUNTRY: USA
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/600,452A
; FILING DATE: 13-FEB-1996
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; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Haile, Lisa A.
; REGISTRATION NUMBER: 38,347
; REFERENCE/DOCKET NUMBER: 07662/005001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 678-5070
; TELEFAX: (619) 678-5099
; TELEX:
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2951 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-600-452A-7

Query Match      8.9%; Score 29.2; DB 2; Length 2951;
Best Local Similarity 62.2%; Pred. No. 5.3;
Matches 46; Conservative 0; Mismatches 28; Indels 0; Gaps 0;

QY 3 GCGCGCAGCGATGATGTGATACCCGAGCGCACCAACAGCGCGCGCGGCAAGAGCG 62
Db 151 GCGCGCAGCGAGCGCGAGGTAGAACAGAGCCCCCGACAGCAATGCCAGCAGGGAATG 92
QY 63 CTTTGAAGTGAATA 76
Db 91 TTTTGGACTGAC 78

RESULT 10
US-09-252-991A-4236/c
; Sequence 4236, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 4236
; LENGTH: 648
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-4236

Query Match      8.7%; Score 28.6; DB 4; Length 648;
Best Local Similarity 54.2%; Pred. No. 4;
Matches 58; Conservative 0; Mismatches 49; Indels 0; Gaps 0;

QY 16 GATGTGATACCCGAGCGCGCACCAACAGCGCGCGGCAAGAGCGCTTTGAAGTGA 75
Db 509 GAGTCGAGAAGTGTACCGCAAGTTCTGCGTGAGATCGAGAAGCGACTGGAAGCA 450
QY 76 AAGTGAATGCAGTAGCCCTCTGGGCTGGGATATTGTGTTGATAA 122
Db 449 GAAGCGGACCTCATGCTGCTGAGCGCGGCTGACGTATGGAATA 403

RESULT 11
US-09-252-991A-9470/c
; Sequence 9470, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
```

```
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 9470
; LENGTH: 723
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-9470

Query Match      8.7%; Score 28.6; DB 4; Length 723;
Best Local Similarity 48.5%; Pred. No. 4.3;
Matches 79; Conservative 0; Mismatches 84; Indels 0; Gaps 0;

QY 10 GCGATGGATGTGGATACCCGAGCGCGCACCAACAGCGCGCGGCAAGAGCGCTTTGAA 69
Db 651 GAGTTGCCAGTCGACGCGGCATCGTCACTCTCCCTGGCAAGCGCGCAACTGCTCGCG 592
QY 70 GTGAAAAGTGAATGCAGTAGCCCTCTGGGCTGGGATATTGTGGTTGATTAACCTGCC 129
Db 591 CGGCACCGAGCGATCGGAGCGCGCTCGAGGACCACTACCGCGCCCTTGATGTTCTCGC 532
QY 130 ATCTGCAGGAACCACTATTGATCTTTGCATAGAAATGTCAAG 172
Db 531 ATGCGCGCGGTCCGGCGTATCCAGGGTGCCATGGAAGNACAG 489

RESULT 12
US-07-598-873-1/c
; Sequence 1, Application US/07598873
; Patent No. 5254800
; GENERAL INFORMATION:
; APPLICANT: BIRD, COLIN R
; APPLICANT: GRIERSON, DONALD
; APPLICANT: RAY, JOHN A
; APPLICANT: SCHUCH, WOLFGANG W
; TITLE OF INVENTION: DNA, CONSTRUCTS, CELLS AND PLANTS
; TITLE OF INVENTION: DERIVED THEREFROM
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CUSHMAN, DARBY & CUSHMAN
; STREET: Eleventh Floor, 1615 L Street, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20036-5601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/598,873
; FILING DATE: 19901019
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: WILSON, MARY J
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-861-3000
; TELEFAX: 202-822-0944
; TELEX: 6714627 CUSH
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1080 base pairs
; TYPE: NUCLEIC ACID
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA to mRNA
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; HYPOTHETICAL: NO
; ORIGINAL SOURCE:
; ORGANISM: Lycopersicon esculentum
; STRAIN: Ailsa Craig
; DEVELOPMENTAL STAGE: Ripening
; US-07-598-873-1
Query Match      8.7%; Score 28.6; DB 1; Length 1080;
Best Local Similarity 61.3%; Pred. No. 5.2;
Matches 46; Conservative 0; Mismatches 29; Indels 0; Gaps 0;

QY 221 TCTGTAACCATGCTTTTTCACCTCCACTGCATCTCTCGTGGCTCAAAACACGACGGTGT 280
Db 742 TCTTTAACTTTCTTGATCAATTCACCTGCATATGTCACCTGGATTGGAACATAACAAACCT 683

QY 281 GTCCATTGGACAACA 295
Db 682 GCTTTTGATACAACA 668

RESULT 14
US-08-396-531-1/c
; Sequence 1, Application US/08396531
; Patent No. 5744364
; GENERAL INFORMATION:
; APPLICANT: BIRD, COLIN R
; APPLICANT: GRIERSON, DONALD
; APPLICANT: RAY, JOHN A
; APPLICANT: SCHUCH, WOLFGANG W
; TITLE OF INVENTION: DNA, CONSTRUCTS, CELLS AND PLANTS
; TITLE OF INVENTION: DERIVED THEREFROM
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CUSHMAN, DARBY & CUSHMAN
; STREET: Ninth Floor, 1100 New York Avenue, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20005-3918
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/396,531
; FILING DATE:
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/847,037
; FILING DATE: 16-APR-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: KOKULIS, PAUL N.
; REGISTRATION NUMBER: 16,773
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-861-3000
; TELEFAX: 202-822-0944
; TELEX: 6714627 CUSH
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1080 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA to mRNA
; HYPOTHETICAL: NO
; ORIGINAL SOURCE:
; ORGANISM: Lycopersicon esculentum
; STRAIN: Ailsa Craig
; DEVELOPMENTAL STAGE: Ripening
; US-08-396-531-1
Query Match      8.7%; Score 28.6; DB 1; Length 1080;
Best Local Similarity 61.3%; Pred. No. 5.2;
Matches 46; Conservative 0; Mismatches 29; Indels 0; Gaps 0;

QY 221 TCTGTAACCATGCTTTTTCACCTCCACTGCATCTCTCGTGGCTCAAAACACGACGGTGT 280
Db 742 TCTTTAACTTTCTTGATCAATTCACCTGCATATGTCACCTGGATTGGAACATAACAAACCT 683

QY 281 GTCCATTGGACAACA 295
Db 682 GCTTTTGATACAACA 668

RESULT 13
US-08-073-425-1/c
; Sequence 1, Application US/08073425
; Patent No. 5569829
; GENERAL INFORMATION:
; APPLICANT: BIRD, COLIN R
; APPLICANT: BONIWELL, JEREMY M.
; APPLICANT: GRIERSON, DONALD
; APPLICANT: RAY, JOHN A
; APPLICANT: SCHUCH, WOLFGANG W
; TITLE OF INVENTION: PLANTS
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CUSHMAN, DARBY & CUSHMAN
; STREET: 1100 New York Avenue, N.W.
; CITY: WASHINGTON
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20005-3918
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/073,425
; FILING DATE: 09-JUN-1993
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: DEEVER, DONALD B.
; REGISTRATION NUMBER: 23,048
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-861-3000
; TELEFAX: 202-822-0944
; TELEX: 6714627 CUSH
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1080 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA to mRNA
; HYPOTHETICAL: NO
; ORIGINAL SOURCE:
; ORGANISM: Lycopersicon esculentum
; STRAIN: Ailsa Craig
; DEVELOPMENTAL STAGE: Ripening
; US-08-073-425-1
Query Match      8.7%; Score 28.6; DB 1; Length 1080;
Best Local Similarity 61.3%; Pred. No. 5.2;
Matches 46; Conservative 0; Mismatches 29; Indels 0; Gaps 0;
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RESULT 15  
 US-09-252-991A-4168/c  
 ; Sequence 4168, Application US/09252991A  
 ; Patent No. 6551795  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Marc J. Rubenfield et al.  
 ; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS  
 ; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS  
 ; FILE REFERENCE: 107196.136  
 ; CURRENT APPLICATION NUMBER: US/09/252,991A  
 ; CURRENT FILING DATE: 1999-02-18  
 ; PRIOR APPLICATION NUMBER: US 60/074,788  
 ; PRIOR FILING DATE: 1998-02-18  
 ; PRIOR APPLICATION NUMBER: US 60/094,190  
 ; PRIOR FILING DATE: 1998-07-27  
 ; NUMBER OF SEQ ID NOS: 33142  
 ; SEQ ID NO 4168  
 ; LENGTH: 1488  
 ; TYPE: DNA  
 ; ORGANISM: Pseudomonas aeruginosa  
 US-09-252-991A-4168

Query Match 8.7%; Score 28.6; DB 4; Length 1488;  
 Best Local Similarity 54.2%; Pred. No. 6.1;  
 Matches 58; Conservative 0; Mismatches 49; Indels 0; Gaps 0;  
 QY 16 GATGTGATACCCGAGCGGACACAGCGCGGCAAGAGCGCTTTGAAGTGAAA 75  
 Db 846 GACGTGCAGAGCTGACCCAGAGTTTCATCGGTGAGATCGAAGGCACTGGAGCCAAA 787  
 QY 76 AAGTGGATGCCAGTAGCCCTCTGGGCGTGGGATATTGTGGTTGATAA 122  
 Db 786 GAAGCGGACCTCATGCTCTCTGAGCGCGGCTGACGTCATGGAATA 740

Search completed: January 22, 2004, 13:55:30  
 Job time : 52 secs

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Result No.	Score	Query		Length	DB	ID	Description
		Match	%				
1	325	99.4	476	11	US-09-918-995-17191		Sequence 17191, A
C 2	321.8	98.4	4543	15	US-10-198-846-11311		Sequence 11311, A
C 3	302.4	92.5	380	10	US-09-960-352-4677		Sequence 4677, Ap
C 4	301.2	92.1	5347	13	US-10-240-965-99		Sequence 99, Appl
C 5	296.8	90.8	5111	15	US-10-205-823-382		Sequence 382, App
C 6	293.6	77.6	3208	9	US-09-780-016-27		Sequence 27, Appl
7	253.6	77.6	3208	15	US-10-214-811-27		Sequence 27, Appl
8	205.8	62.9	4329	11	US-09-918-995-14771		Sequence 14771, A
9	183.8	56.2	17561	15	US-10-017-721-3		Sequence 3, Appl
10	173	52.9	390	9	US-09-770-791-20		Sequence 20, Appl
C 11	157.4	48.1	418	9	US-09-963-436-220		Sequence 220, App
C 12	138.8	42.4	415	15	US-10-198-846-2493		Sequence 2493, Ap
C 13	102.2	31.3	812	12	US-10-264-049-751		Sequence 751, App
C 14	76.4	23.4	271	9	US-09-294-093B-735		Sequence 735, App
15	76	23.2	836	10	US-09-764-864-39		Sequence 39, Appl

Db 194 CTGTGCCATCTGCAGGAACACATTAATGATCTTTTCATAGATGTCAGAGTCAAGCTAACCCAGGC 253  
Qy 183 GTCCGCTACTTCAGAGAGTGTACTGTCCGATGGGAGTCTGTAAACCATGCTTTTTCACCTT 242  
Db 254 GTCCGCTACTTCAGAGAGTGTACTGTCCGATGGGAGTCTGTAAACCATGCTTTTTCACCTT 313  
Qy 243 CCACTGCATCTCTCGCTGGCTCAAAACACAGCAGAGTGTGTCCATTGGACAAACAGAGAGTG 302  
Db 314 CCACTGCATCTCTCGCTGGCTCAAAACACAGCAGAGTGTGTCCATTGGACAAACAGAGAGTG 373  
Qy 303 GGAATTCCTCAAAAGTATGGGCACCTAG 327  
Db 374 GGAATTCCTCAAAAGTATGGGCACCTAG 398

RESULT 2

US-10-198-846-11311/c  
; Sequence 11311, Application US/10198846  
; Publication No. US20030099974A1  
; GENERAL INFORMATION:  
; APPLICANT: Lillie, James  
; APPLICANT: Xu, Yongyao  
; APPLICANT: Wang, Youzhen  
; APPLICANT: Steinmann, Kathleen  
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS  
; TITLE OF INVENTION: FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND  
; TITLE OF INVENTION: THERAPY OF BREAST CANCER  
; FILE REFERENCE: MRI-049  
; CURRENT APPLICATION NUMBER: US/10/198,846  
; CURRENT FILING DATE: 2002-07-18  
; PRIOR APPLICATION NUMBER: 60/306,220  
; PRIOR FILING DATE: 2001-07-18  
; NUMBER OF SEQ ID NOS: 14084  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 11311  
; LENGTH: 4543  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-198-846-11311

Query Match 98.4%; Score 321.8; DB 15; Length 4543;  
Best Local Similarity 99.4%; Pred. No. 7.4e-104;  
Matches 323; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 3 GCGCGCAGCATGGATGTGGATACCCCGAGCGGCACCAACAGCGCGCGCGGCAAGAGCG 62  
Db 1089 GCGCGCAGCATGGATGTGGATACCCCGAGCGGCACCAACAGCGCGCGCGGCAAGAGCG 1030  
Qy 63 CTTTGAAGTGAAGAGTGAATGCAGTACGCCCTCTGGGCTGGGATATTGTGTTGATTA 122  
Db 1029 CTTTGAAGTGAAGAGTGAATGCAGTACGCCCTCTGGGCTGGGATATTGTGTTGATTA 970  
Qy 123 CTGTGCCATCTGCAGGAACACACATTAATGATCTTTGCATAGATGTCAAGCTAACCCAGGC 182  
Db 969 CTGTGCCATCTGCAGGAACACACATTAATGATCTTTGCATAGATGTCAAGCTAACCCAGGC 910  
Qy 183 GTCCGCTACTTCAGAGAGTGTACTGTCCGATGGGAGTCTGTAAACCATGCTTTTTCACCTT 242  
Db 909 GTCCGCTACTTCAGAGAGTGTACTGTCCGATGGGAGTCTGTAAACCATGCTTTTTCACCTT 850  
Qy 243 CCACTGCATCTCTCGCTGGCTCAAAACACAGCAGAGTGTGTCCATTGGACAAACAGAGAGTG 302  
Db 849 CCACTGCATCTCTCGCTGGCTCAAAACACAGCAGAGTGTGTCCATTGGACAAACAGAGAGTG 790  
Qy 303 GGAATTCCTCAAAAGTATGGGCACCTAG 327  
Db 789 GGAATTCCTCAAAAGTATGGGCACCTAG 765

RESULT 3

US-09-960-352-4677  
; Sequence 4677, Application US/09960352

; Patent No. US20020137139A1  
; GENERAL INFORMATION:  
; APPLICANT: Warren, Wesley C.  
; APPLICANT: Tao, Nengbing  
; APPLICANT: Byatt, John C.  
; APPLICANT: Mathialagan, Nagappan  
; TITLE OF INVENTION: MUSCLE AND FAT DEPOSITION  
; FILE REFERENCE: 16511.006/37-21(10298)C  
; CURRENT APPLICATION NUMBER: US/09/960,352  
; CURRENT FILING DATE: 2001-09-24  
; NUMBER OF SEQ ID NOS: 15112  
; SEQ ID NO 4677  
; LENGTH: 380  
; TYPE: DNA  
; ORGANISM: Bos taurus  
; OTHER INFORMATION: Clone ID: 20-LIB34-034-Q1-E1-E7  
US-09-960-352-4677

Query Match 92.5%; Score 302.4; DB 10; Length 380;  
Best Local Similarity 96.6%; Pred. No. 2e-97;  
Matches 309; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

Qy 8 CAGCGATGATGTGGATACCCCGAGCGGCACCAACAGCGCGCGGCAAGAGCGCTTTG 67  
Db 2 CAGCGATGATGTGGATACCCCGAGCGGCACCAACAGCGCGCGGCAAGAGCGCTTTG 61  
Qy 68 AAGTGAAGAGTGAATGCAGTAGCCCTCTGGGCTGGGATATTGTGTTGATACTGTG 127  
Db 62 AAGTGAAGAGTGAATGCAGTAGCCCTCTGGGCTGGGATATTGTGTTGATACTGTG 121  
Qy 128 CCATCTGCAGGAACACACATTAATGATCTTTGCATAGATGTCAAGCTAACCCAGGCGTCCG 187  
Db 122 CCATCTGCAGGAACACACATTAATGATCTTTGCATAGATGTCAAGCTAACCCAGGCGTCCG 181  
Qy 188 CTACTTCAGAGAGTGTACTGTGCGATGGGAGTCTGTAAACCATGCTTTTTCACCT 247  
Db 182 CTACTTCAGAGAGTGTACTGTGCGTGGCGGTCTGTAAACCATGCTTTTTCACCT 241  
Qy 248 GCATCTCTCGCTGGCTCAAAACACAGCAGAGTGTGTCCATTGGACAAACAGAGAGTGGAAT 307  
Db 242 GCATCTCTCGCTGGCTCAAAACACAGCAGAGTGTGTCCGTTGGACAAACAGAGAGTGGAAT 301  
Qy 308 TCCAAAAGTATGGGCACCTAG 327  
Db 302 TCCAAAAGTATGGGCACCTAG 321

RESULT 4

US-10-240-965-99/c  
; Sequence 99, Application US/10240965  
; Publication No. US20030165924A1  
; GENERAL INFORMATION:  
; APPLICANT: INCYTE GENOMICS, INC.  
; APPLICANT: SHIFFMAN, Dov  
; APPLICANT: SOMOGYI, Roland  
; APPLICANT: LAWN, Richard M.  
; APPLICANT: SEILHAMER, Jeffrey J.  
; APPLICANT: PORTER, Gordon J.  
; APPLICANT: MIKITA, Thomas  
; APPLICANT: TAI, Julie  
; TITLE OF INVENTION: GENES EXPRESSED IN FOAM CELL DIFFERENTIATION  
; FILE REFERENCE: PA-0025 PCT  
; CURRENT APPLICATION NUMBER: US/10/240,965  
; CURRENT FILING DATE: 2002-10-04  
; PRIOR APPLICATION NUMBER: 60/195,106  
; PRIOR FILING DATE: 2000-04-05  
; NUMBER OF SEQ ID NOS: 276  
; SOFTWARE: PERL Program  
; SEQ ID NO 99  
; LENGTH: 5347  
; TYPE: DNA  
; ORGANISM: Homo sapiens

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; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No. US20030165924A1 364940.19
US-10-240-965-99

Query Match      92.1%; Score 301.2; DB 13; Length 5347;
Best Local Similarity 98.7%; Pred. No. 1.8e-96;
Matches 314; Conservative 0; Mismatches 3; Indels 1; Gaps 1;

QY 3 GCGCGCAGCGATGGATGTGGATACCCCGAGCGGCACCAACAGCGGCGC-GGGCAAGAAGC 61
DB 519 GCGCGCAGCGATGGATGTGGATACCCCGAGCGGCACCAACAGCGGCGGCGCAAGAAGC 460

QY 62 GCTTTGAAGTGAAGAGTGAATGCAGTAGCCCTCTGGGCTGGGATATTGGTTGATA 121
DB 459 GCTTTGAAGTGAAGAGTGAATGCAGTAGCCCTCTGGGCTGGGATATTGGTTGATA 400

QY 122 ACTGTGCCATCTGCAGGAACCAATTATGGATCTTTGCATAGATGTCAAGCTAACCCAGG 181
DB 399 ACTGTGCCATCTGCAGGAACCAATTATGGATCTTTGCATAGATGTCAAGCTAACCCAGG 340

QY 182 CGTCCGCTACTTCAGAAAGTGTACTGTGCATGGGAGTCTGTAAACCATGCTTTTCACT 241
DB 339 CGTCCGCTACTTCAGAAAGTGTACTGTGCATGGGAGTCTGTAAACCATGCTTTTCACT 280

QY 242 TCCACTGCATCTCTCGCTGCTCAAAACACAGCAGGTGTGTCCATTTGGACAAACAGAGGT 301
DB 279 TCCACTGCATCTCTCGCTGCTCAAAACACAGCAGGTGTGTCCATTTGGACAAACAGAGGT 220

QY 302 GGGAAATCCAAAAGTAGT 319
DB 219 GGGAAATCCAAAAGTAGT 202

RESULT 5
US-10-205-823-382/c
; Sequence 382, Application US/10205823
; Publication No. US20030108963A1
; GENERAL INFORMATION:
; APPLICANT: Schlegel, Robert
; APPLICANT: Monahan, John E.
; APPLICANT: Endege, Wilson O.
; APPLICANT: Gannavarapu, Manjula
; APPLICANT: Gorbacheva, Bella
; APPLICANT: Hoersch, Sebastian
; APPLICANT: Kamatkar, Shubhangi
; APPLICANT: Wensey, Angela M.
; APPLICANT: Glatt, Karen
; APPLICANT: Zhao, Xumei
; APPLICANT: Anderson, Dustin
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND
; TITLE OF INVENTION: METHODS FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND
; TITLE OF INVENTION: THERAPY OF PROSTATE CANCER
; FILE REFERENCE: MRI-044
; CURRENT APPLICATION NUMBER: US/10/205,823
; CURRENT FILING DATE: 2002-07-25
; PRIOR APPLICATION NUMBER: 60/307,982
; PRIOR FILING DATE: 2001-07-25
; PRIOR APPLICATION NUMBER: 60/314,356
; PRIOR FILING DATE: 2001-08-22
; PRIOR APPLICATION NUMBER: 60/325,020
; PRIOR FILING DATE: 2001-09-25
; PRIOR APPLICATION NUMBER: 60/341,746
; PRIOR FILING DATE: 2001-12-12
; PRIOR APPLICATION NUMBER: 60/362,158
; PRIOR FILING DATE: 2002-03-05
; NUMBER OF SEQ ID NOS: 455
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 382
; LENGTH: 5111
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-205-823-382

Query Match      90.8%; Score 296.8; DB 15; Length 5111;
Best Local Similarity 99.3%; Pred. No. 6.7e-95;
Matches 298; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 GCGCGCAGCGATGGATGTGGATACCCCGAGCGGCACCAACAGCGGCGGCAAGAAGCG 62
DB 300 GCGCGCAGCGATGGATGTGGATACCCCGAGCGGCACCAACAGCGGCGGCAAGAAGCG 241

QY 63 CTTTGAAGTGAAGAGTGAATGCAGTAGCCCTCTGGGCTGGGATATTGGTTGATAA 122
DB 240 CTTTGAAGTGAAGAGTGAATGCAGTAGCCCTCTGGGCTGGGATATTGGTTGATAA 181

QY 123 CTGTGCCATCTGCAGGAACCAATTATGGATCTTTGCATAGATGTCAAGCTAACCCAGC 182
DB 180 CTGTGCCATCTGCAGGAACCAATTATGGATCTTTGCATAGATGTCAAGCTAACCCAGC 121

QY 183 GTCCGCTACTTCAGAAAGTGTACTGTGCATGGGAGTCTGTAAACCATGCTTTTCACTT 242
DB 120 GTCCGCTACTTCAGAAAGTGTACTGTGCATGGGAGTCTGTAAACCATGCTTTTCACTT 61

QY 243 CCACTGCATCTCTCGCTGCTCAAAACACAGCAGGTGTGTCCATTTGGACAAACAGAGGTG 302
DB 60 CCACTGCATCTCTCGCTGCTCAAAACACAGCAGGTGTGTCCATTTGGACAAACAGAGGTG 1

RESULT 6
US-09-780-016-27
; Sequence 27, Application US/09780016
; Patent No. US20020004591A1
; GENERAL INFORMATION:
; APPLICANT: Donoho, Gregory
; APPLICANT: Scoville, John
; APPLICANT: Turner, C. Alexander Jr.
; APPLICANT: Friedrich, Glenn
; APPLICANT: Abuin, Alejandro
; APPLICANT: Zambrowicz, Brian
; APPLICANT: Sands, Arthur T.
; TITLE OF INVENTION: Polynucleotides Encoding the Same
; FILE REFERENCE: LEX-0132-USA
; CURRENT APPLICATION NUMBER: US/09/780,016
; CURRENT FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: US 60/181,294
; PRIOR FILING DATE: 2000-02-11
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 27
; LENGTH: 3208
; TYPE: DNA
; ORGANISM: homo sapiens
US-09-780-016-27

Query Match      77.6%; Score 253.6; DB 9; Length 3208;
Best Local Similarity 98.5%; Pred. No. 1.5e-79;
Matches 256; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 68 AAGTGAAGAGTGAATGCAGTAGCCCTCTGGGCTGGGATATTGGTTGATAACTGTG 127
DB 2765 AAAAAAAAAAATGGAATGCAGTAGCCCTCTGGGCTGGGATATTGGTTGATAACTGTG 2824

QY 128 CCATCTGCAGGAACCAATTATGGATCTTTGCATAGATGTCAAGCTAACCCAGCGTCCG 187
DB 2825 CCATCTGCAGGAACCAATTATGGATCTTTGCATAGATGTCAAGCTAACCCAGCGTCCG 2884

QY 188 CTACTTTCAGAGAGTGTACTGTGGATGGGAGTCTGTAAACCATGCTTTTCACTTCCACT 247
DB 2885 CTACTTTCAGAGAGTGTACTGTGGATGGGAGTCTGTAAACCATGCTTTTCACTTCCACT 2944

QY 248 GCATCTCTCGCTGGCTCAAAACACAGCAGGTGTGTCCATTTGGACAAACAGAGTGGAAAT 307
DB 2945 GCATCTCTCGCTGGCTCAAAACACAGCAGGTGTGTCCATTTGGACAAACAGAGTGGAAAT 3004
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Db 59683 TCACCTT-CACCTGCTCTCTCACTGGCTCAAAACACACAGCTGTGCTGTTGGACACAG 59741  
QY 297 AGAGTGGGAATTCCTCAAGATGATGGCAGCTAG 327  
Db 59742 ACAATAGGAAATCCCAAGATGATGGACACAG 59772

RESULT 10  
US-09-770-791-20  
; Sequence 20, Application US/09770791  
; Patent No. US20020082014A1  
; GENERAL INFORMATION:  
; APPLICANT: Gorlach, Jorn  
; APPLICANT: An, Yong-Qiang  
; APPLICANT: Hamilton, Carol M.  
; APPLICANT: Price, Jennifer L.  
; APPLICANT: Raines, Tracy M.  
; APPLICANT: Yu, Yang  
; APPLICANT: Rameaka, Joshua G.  
; APPLICANT: Page, Amy  
; APPLICANT: Matthew, Abraham V.  
; APPLICANT: Ledford, Brooke L.  
; APPLICANT: Woessner, Jeffrey P.  
; APPLICANT: Haas, William David  
; APPLICANT: Garcia, Carlos A.  
; APPLICANT: Krickler, Maja  
; APPLICANT: Slader, Ted  
; APPLICANT: Davis, Keith R.  
; APPLICANT: Allen, Keith  
; APPLICANT: Hoffman, Patrick  
; APPLICANT: Hurban, Patrick  
; TITLE OF INVENTION: Expressed Sequences of Arabidopsis  
; FILE REFERENCE: 2029 (PARA-018PRV)  
; CURRENT APPLICATION NUMBER: US/09/770,791  
; CURRENT FILING DATE: 2001-01-26  
; PRIOR APPLICATION NUMBER: 60/178,480  
; PRIOR FILING DATE: 2000-01-27  
; NUMBER OF SEQ ID NOS: 999  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 20  
; LENGTH: 390  
; TYPE: DNA  
; ORGANISM: Arabidopsis thaliana

US-09-770-791-20

Query Match 52.9%; Score 173; DB 9; Length 390;  
Best Local Similarity 77.7%; Pred. No. 3.7e-51;  
Matches 209; Conservative 0; Mismatches 60; Indels 0; Gaps 0;

QY 58 AAGCGCTTTGAAGTGAAAAGTGAATGAGTACGCTGAGTGGCTGGGATATTTGGTT 117  
Db 110 AAGCGATTCGAAATTAAGAAAGTGGAGCGGCTGTCTCTGGGCTGGGATATCGTTGT 169  
QY 118 GATACTGTGCCATCTGCAGGAACACATATTAGGATCTTTGCATAGAAATGTCAGACTAAC 177  
Db 170 GACAAGTGGCGATCTGCAGAAACACATCATGATCTTTGTATCGAGTGCAGGCTAAT 229  
QY 178 CAGGCGTCGGCTACTTCAGAAAGTGTACTGTGCGATGGGAGTCTGTAAACCATGCTTTT 237  
Db 230 CAGGCGAGTGCACAAAGTGAAGAGTGCATGTAGCTTGGGGGTTTGCATACAGCGCTTC 289  
QY 238 CACTTCCACTGATCTCTCGCTGGCTCAAAACACAGAGTGTGTCATGGACACAGA 297  
Db 290 CACTTTCATGATCAGCAGATGGCTAAAGATCTCGTCAAGTTGTGCCATTGGATAACAGT 349  
QY 298 GAGTGGGAATTCCTCAAGATGATGGCAGTACTA 326  
Db 350 GAGTGGGAGTTTCAGNAATATGGTCACTA 378

RESULT 11

US-09-962-436-220/c  
; Sequence 220, Application US/09962436  
; Patent No. US20020081301A1  
; GENERAL INFORMATION:  
; APPLICANT: Sopret, Daniel  
; TITLE OF INVENTION: Cancer Gene Determination and Therapeutic Screening Using Signatu  
; TITLE OF INVENTION: Sets  
; FILE REFERENCE: 689290-75  
; CURRENT APPLICATION NUMBER: US/09/962,436  
; CURRENT FILING DATE: 2001-09-25  
; PRIOR APPLICATION NUMBER: US/60/235,082  
; PRIOR FILING DATE: 2000-09-25  
; PRIOR APPLICATION NUMBER: US/60/234,924  
; PRIOR FILING DATE: 2000-09-25  
; NUMBER OF SEQ ID NOS: 568  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 220  
; LENGTH: 418  
; TYPE: DNA  
; ORGANISM: Homo sapiens

US-09-962-436-220

Query Match 48.1%; Score 157.4; DB 9; Length 418;  
Best Local Similarity 85.4%; Pred. No. 1.4e-45;  
Matches 199; Conservative 0; Mismatches 31; Indels 3; Gaps 2;

QY 95 TCTGGGCTGGGATATTCTGTGATAACTGTGTCATCTGCGCATCTGCAGGAACACATTTATGGATC 154  
Db 417 TCTGGGCTGGGATATTCTGTGATAACTGTGTCATCTGCGCATCTGCAGGAATCACAGCATGGATC 358  
QY 155 TTTGCATAGATGTCAACCTAACCAAGCGTCCGTCTTCACTTCCACTGATCTCTCGCTGGCTCAAAACACGAC 214  
Db 357 --TGCATTGAATGTCAAGCTAACCAAGAGTCTGCACCTTCAGAAAGTGTGTACCGTTGCAC 300  
QY 215 GGGAGTCTGTAAACCATCTTTTCACTTCCACTGATCTCTCGCTGGCTCAAAACACGAC 274  
Db 299 GGGAGCGCTGTAAACCGTCTTTTCACTT--CACTGTCTCTCTCACCTGGCTCAAAACACACAC 241  
QY 275 AGGTGTGTCCATTGGACAAACAGAGAGTGGGAATTCCTCAAAAGTATGGCAGCTAG 327  
Db 240 AGCTGTGCTGTGGACAAACAGACATAGGAATTCCTCAAAAGTATGGACACACAG 188

RESULT 12

US-10-198-846-2493  
; Sequence 2493, Application US/10198846  
; Publication No. US20030099974A1  
; GENERAL INFORMATION:  
; APPLICANT: Lillie, James  
; APPLICANT: Xu, Yongyao  
; APPLICANT: Wang, Youzhen  
; APPLICANT: Steinmann, Kathleen  
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS  
; TITLE OF INVENTION: FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND  
; TITLE OF INVENTION: THERAPY OF BREAST CANCER  
; FILE REFERENCE: MRI-049  
; CURRENT APPLICATION NUMBER: US/10/198,846  
; CURRENT FILING DATE: 2002-07-18  
; PRIOR APPLICATION NUMBER: 60/306,220  
; PRIOR FILING DATE: 2001-07-18  
; NUMBER OF SEQ ID NOS: 14084  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 2493  
; LENGTH: 415  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: misc\_feature  
; LOCATION: 5  
; OTHER INFORMATION: n = A,T,C or G

US-10-198-846-2493

Query Match 42.4%; Score 138.8; DB 15; Length 415;



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OM protein - nucleic search, using frame\_plus\_p2n model

Run on: January 22, 2004, 13:34:15 ; Search time 55 Seconds

(without alignments)

866.716 Million cell updates/sec

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Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 569978 seqs, 220691566 residues

Total number of hits satisfying chosen parameters: 1139956

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Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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-LIST=45 -DOCALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15  
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-NO\_MMAP -LARGEQUERY -NEG\_SCORES=0 -WAIT -DSFLOCK=100 -LONGLOG  
-DEV TIMEOUT=120 -WARN\_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6  
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Issued Patents NA:\*

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3: /cgn2\_6/prodata/1/ina/6A COMB.seq:\*  
4: /cgn2\_6/prodata/1/ina/6B COMB.seq:\*  
5: /cgn2\_6/prodata/1/ina/PCBUS COMB.seq:\*  
6: /cgn2\_6/prodata/1/ina/backfiles1.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	501.5	81.4	3208	4	US-09-780-016-27
2	262.5	42.6	301	4	US-09-313-294A-492
3	217	35.2	648	4	US-09-599-360B-27
4	90	14.6	8438	1	US-07-945-283-1
5	85	13.8	2339	3	US-09-268-140-11
6	85	13.8	2505	3	US-09-268-140-1
7	85	13.8	2517	3	US-09-268-140-7
8	81	13.5	315	4	US-09-325-932A-4
9	81.5	13.2	4259	2	US-08-816-155B-2
10	81.5	13.2	4259	3	US-09-079-587-2
11	80.5	13.1	804	3	US-08-998-416-881
12	80	13.0	944	2	US-08-786-606-4

13	80	13.0	1112	2	US-08-933-750C-97	Sequence 97, Appl
14	80	13.0	1112	3	US-09-234-613-97	Sequence 97, Appl
15	79.5	12.9	1683	1	US-07-945-283-3	Sequence 3, Appl
16	79	12.8	1470	4	US-09-663-600A-153	Sequence 153, Appl
17	79	12.8	1544	2	US-08-867-057-2	Sequence 2, Appl
18	79	12.8	1544	2	US-08-128-389-2	Sequence 2, Appl
19	79	12.8	1570	4	US-09-663-600A-59	Sequence 59, Appl
20	78	12.7	278	4	US-09-313-294A-756	Sequence 756, Appl
21	78	12.7	2146	4	US-09-620-312D-443	Sequence 443, Appl
22	77.5	12.6	617	4	US-09-280-116-115	Sequence 115, Appl
23	77.5	12.6	1830121	4	US-09-557-884-1	Sequence 1, Appl
24	77.5	12.6	1830121	4	US-09-643-990A-1	Sequence 1, Appl
25	76	12.3	621	4	US-09-364-206-28	Sequence 28, Appl
26	76	12.3	3911	4	US-09-423-890-1	Sequence 1, Appl
27	76	12.3	4693	3	US-09-359-756-1	Sequence 1, Appl
28	76	12.3	5253	4	US-09-423-890-7	Sequence 7, Appl
29	76	12.3	5539	4	US-08-628-829-3	Sequence 3, Appl
30	75.5	12.3	1355	4	US-09-599-360B-64	Sequence 64, Appl
31	74.5	12.1	900	4	US-09-328-352-1185	Sequence 1185, Appl
32	74.5	12.1	1114	4	US-09-690-454-39	Sequence 39, Appl
33	74.5	12.1	1251	4	US-09-205-258-156	Sequence 156, Appl
34	74.5	12.1	1253	2	US-08-786-606-6	Sequence 6, Appl
35	74.5	12.1	1253	4	US-09-016-434-5	Sequence 5, Appl
36	74.5	12.1	1831	6	5215881-1	Patent No. 5215881
37	74.5	12.1	1831	6	5215881-3	Patent No. 5215881
38	74.5	12.1	2481	4	US-09-894-998A-35	Sequence 35, Appl
39	74	12.0	266	4	US-09-313-294A-1763	Sequence 1763, Appl
40	74	12.0	148567	4	US-09-801-876B-3	Sequence 3, Appl
41	73	11.9	1397	3	US-08-946-026-17	Sequence 17, Appl
42	73	11.9	1656	3	US-08-699-103B-7	Sequence 7, Appl
43	73	11.9	1656	4	US-09-229-059-7	Sequence 7, Appl
44	73	11.9	1656	4	US-09-628-133-7	Sequence 7, Appl
45	72.5	11.8	666	1	US-08-018-977C-2	Sequence 2, Appl

ALIGNMENTS

RESULT 1  
US-09-780-016-27  
; Sequence 27, Application US/09780016  
; Patent No. 6509456  
; GENERAL INFORMATION:  
; APPLICANT: Donoho, Gregory  
; APPLICANT: Scoville, John  
; APPLICANT: Turner, C. Alexander Jr.  
; APPLICANT: Friedrich, Glenn  
; APPLICANT: Abuin, Alejandro  
; APPLICANT: Zambrowicz, Brian  
; APPLICANT: Sands, Arthur T.  
; TITLE OF INVENTION: No. 6509456el Human Proteases and  
; FILE OF INVENTION: Polynucleotides Encoding the Same  
; FILE REFERENCE: LEX-0132-USA  
; CURRENT APPLICATION NUMBER: US/09/780,016  
; PRIOR FILING DATE: 2001-02-09  
; PRIOR APPLICATION NUMBER: US 60/181,294  
; PRIOR FILING DATE: 2000-02-11  
; NUMBER OF SEQ ID NOS: 27  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 27  
; LENGTH: 3208  
; TYPE: DNA  
; ORGANISM: homo sapiens  
US-09-780-016-27  
  
Alignment Scores:  
Pred. No.: 5.03e-53  
Score: 501.50  
Percent Similarity: 95.70%  
Best Local Similarity: 94.62%  
Query Match: 81.41%  
Indels: 3  
Gaps: 1  
Length: 3208  
Matches: 88  
Conservative: 1  
Mismatches: 1  
Indels: 3  
Gaps: 1  
US-09-541-462B-2 (1-108) x US-09-780-016-27 (1-3208)

```
; Patent No. 6548633
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Bougueleret, L.
; APPLICANT: Jobert, S.
; TITLE OF INVENTION: Complementary DNA's Encoding Proteins with Signal Peptides
; FILE REFERENCE: GENSET.050CP3
; CURRENT APPLICATION NUMBER: US/09/599,360B
; CURRENT FILING DATE: 2000-06-21
; PRIOR APPLICATION NUMBER: 60/113,686
; PRIOR FILING DATE: 1998-12-22
; PRIOR APPLICATION NUMBER: 60/141,032
; PRIOR FILING DATE: 1999-06-25
; PRIOR APPLICATION NUMBER: 09/469,099
; PRIOR FILING DATE: 1999-12-21
; NUMBER OF SEQ ID NOS: 123
; SOFTWARE: Patent.pm
; SEQ ID NO 27
; LENGTH: 648
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 187..438
; NAME/KEY: polyA signal
; LOCATION: 612..617
; NAME/KEY: polyA site
; LOCATION: 632..648
; US-09-599-360B-27

Alignment Scores:
Pred. No.: 2,79e-18 Length: 648
Score: 217.00 Matches: 43
Percent Similarity: 44.53% Conservative: 18
Best Local Similarity: 31.39% Mismatches: 40
Query Match: 35.23% Indels: 36
DB: 4 Gaps: 3

US-09-541-462B-2 (1-108) x US-09-599-360B-27 (1-648)
QY 2 AlaAlaMetAspValAspThrProSerGlyThrAsnSerGlyAlaGlyLysLysArg 21
Db 49 GCGCGCACTGTGGTCTTTTATACCTTCCCGCGGAGCGCGGCTGCCAACGGAAG 108
QY 22 PheGlu----- 23
Db 109 GCGGAGACGAGATTTCGTCACTGTGGCCAGGCCCATTTGAGATCTTTGAAGATATCCTCA 168
QY 24 -----ValLysLysTrpAsnAlaValAlaLeuTrp 33
Db 169 ACGTCAGGCTCTGCTGCCATGAAGGTGAAGATTAGTGTGGAACGGCGTGGCCACTTGG 228
QY 34 AlaTrpAspIleValValAspAsnCysAlaIleCysArgAsnHisIleMetAspLeuCys 53
Db 229 CTCCTGGTGGCGCAACGATGAGAACTGTGTCATCTCGAGCATGGCATTAAACGGATGCTGC 288
QY 54 IleGluCysGlnAlaAsnGlnAlaSerAlaThrSerGluGluCysThrValAlaTrpGly 73
Db 289 CTTGACTGCAAG-----GTGCGCGCGGAGCATGCCCGCTGTGTGGGGC 333
QY 74 ValCysAsnHisAlaPheHisPheHisCysIleSerArgTrpLeuLysThrArgGlnVal 93
Db 334 CAGTCTCTCCACTGTCTCCACATGATTCATCTCAAGTGGCTGCACGACGACGAGGTG 393
QY 94 -----CysProLeuAspAsnArgGluTrpGluPheGlnLysTrpGly 107
Db 394 CAGCAGCACTGCCCATGTGCCCGCAGGAATGGAAGTTCAGGAGTGAAGGC 444

RESULT 4
US-07-945-283-1/c
; Sequence 1, Application US/07945283
; Patent No. 5352596
; GENERAL INFORMATION:

; 16 GlyAlaGlyLysLysArgPheGluValLysLysTrpAsnAlaValAlaLeuTrpAlaTrp 35
; 2752 GGAGCATATAAAAAAAAA-----AAAATGAATGCAGTAGCCCTCTGGGCTGG 2802
; 36 AspIleValValAspAsnCysAlaIleCysArgAsnHisIleMetAspLeuCysIleGlu 55
; 2803 GATATTGTGGTTGATACTGTGCATCTCGCAGGAACCATATTATGATCTTTGCATAGAA 2862
; 56 CysGlnAlaAsnGlnAlaSerAlaThrSerGluGluCysThrValAlaTrpGlyValCys 75
; 2863 TGTCAAGCTTAACAGCGCTCCGCTACTTCAGAGAGTGTACTGTCCATGGGAGTCTGT 2922
; 76 AsnHisAlaPheHisPheHisCysIleSerArgTrpLeuLysThrArgGlnValCysPro 95
; 2923 AACCATGCTTTTCACTTCCACTGTCATCTCTCGCTGGCTCAAAACACGACAGGTGTGCTCA 2982
; 96 LeuAspAsnArgLysTrpGluPheGlnLysTrpGlyHis 108
; 2983 TTGGACAACAGAGAGTGGGAATTCACAAAGATATGGGCAC 3021

RESULT 2
US-09-313-294A-492
; Sequence 492, Application US/09313294A
; Patent No. 6476212
; GENERAL INFORMATION:
; APPLICANT: Lalgudi, Raghunath V.
; APPLICANT: Ito, Laura Y.
; APPLICANT: Sherman, Bradley K.
; TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES DERIVED FROM CORN EAR
; FILE REFERENCE: PL-0017 US
; CURRENT APPLICATION NUMBER: US/09/313,294A
; CURRENT FILING DATE: 1999-05-14
; NUMBER OF SEQ ID NOS: 7600
; SOFTWARE: PERL Program
; SEQ ID NO 492
; LENGTH: 301
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No. 6476212 700549333H1
; US-09-313-294A-492

Alignment Scores:
Pred. No.: 1,91e-24 Length: 301
Score: 262.50 Matches: 51
Percent Similarity: 71.43% Conservative: 4
Best Local Similarity: 66.23% Mismatches: 7
Query Match: 42.61% Indels: 15
DB: 4 Gaps: 2

US-09-541-462B-2 (1-108) x US-09-313-294A-492 (1-301)
QY 3 AlaAlaMetAspValAsp-----ThrProSerGlyThrAsnSer 15
Db 70 TCCGCCATGGAGACCGACATCAACGCCCGCGCGCCGCCCGCCCGCCCGCGCGGATCC 129
QY 16 GlyAlaGly-----LysLysArgPheGluValLysLysTrp 27
Db 130 TCTGGCGCGGTCGCTCTCTCCCGCAAGCCCAACAGCGCTTCGAGATCAAGAAGTGG 189
QY 28 AsnAlaValAlaLeuTrpAlaTrpAspIleValValAspAsnCysAlaIleCysArgAsn 47
Db 190 AACGCCGCTCGCGCTCTGGCGATGGGATATCGTGTGCAACTGTGGCTATCTGCGCGAAC 249
QY 48 HisIleMetAspLeuCysIleGluCysGlnAlaAsnGlnAlaSerAlaThr 64
Db 250 CACATCATGATCATGATCGATCGAGTCCAGCGGACCAACAGCCAGCGCGACC 300

RESULT 3
US-09-599-360B-27
; Sequence 27, Application US/09599360B
```

```
; Patent No. 6548633
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Bougueleret, L.
; APPLICANT: Jobert, S.
; TITLE OF INVENTION: Complementary DNA's Encoding Proteins with Signal Peptides
; FILE REFERENCE: GENSET.050CP3
; CURRENT APPLICATION NUMBER: US/09/599,360B
; CURRENT FILING DATE: 2000-06-21
; PRIOR APPLICATION NUMBER: 60/113,686
; PRIOR FILING DATE: 1998-12-22
; PRIOR APPLICATION NUMBER: 60/141,032
; PRIOR FILING DATE: 1999-06-25
; PRIOR APPLICATION NUMBER: 09/469,099
; PRIOR FILING DATE: 1999-12-21
; NUMBER OF SEQ ID NOS: 123
; SOFTWARE: Patent.pm
; SEQ ID NO 27
; LENGTH: 648
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 187..438
; NAME/KEY: polyA signal
; LOCATION: 612..617
; NAME/KEY: polyA site
; LOCATION: 632..648
; US-09-599-360B-27

Alignment Scores:
Pred. No.: 2,79e-18 Length: 648
Score: 217.00 Matches: 43
Percent Similarity: 44.53% Conservative: 18
Best Local Similarity: 31.39% Mismatches: 40
Query Match: 35.23% Indels: 36
DB: 4 Gaps: 3

US-09-541-462B-2 (1-108) x US-09-599-360B-27 (1-648)
QY 2 AlaAlaMetAspValAspThrProSerGlyThrAsnSerGlyAlaGlyLysLysArg 21
Db 49 GCGCGCACTGTGGTCTTTTATACCTTCCCGCGGAGCGCGGCTGCCAACGGAAG 108
QY 22 PheGlu----- 23
Db 109 GCGGAGACGAGATTTCGTCACTGTGGCCAGGCCCATTTGAGATCTTTGAAGATATCCTCA 168
QY 24 -----ValLysLysTrpAsnAlaValAlaLeuTrp 33
Db 169 ACGTCAGGCTCTGCTGCCATGAAGGTGAAGATTAGTGTGGAACGGCGTGGCCACTTGG 228
QY 34 AlaTrpAspIleValValAspAsnCysAlaIleCysArgAsnHisIleMetAspLeuCys 53
Db 229 CTCCTGGTGGCGCAACGATGAGAACTGTGTCATCTCGAGCATGGCATTAAACGGATGCTGC 288
QY 54 IleGluCysGlnAlaAsnGlnAlaSerAlaThrSerGluGluCysThrValAlaTrpGly 73
Db 289 CTTGACTGCAAG-----GTGCGCGCGGAGCATGCCCGCTGTGTGGGGC 333
QY 74 ValCysAsnHisAlaPheHisPheHisCysIleSerArgTrpLeuLysThrArgGlnVal 93
Db 334 CAGTCTCTCCACTGTCTCCACATGATTCATCTCAAGTGGCTGCACGACGACGAGGTG 393
QY 94 -----CysProLeuAspAsnArgGluTrpGluPheGlnLysTrpGly 107
Db 394 CAGCAGCACTGCCCATGTGCCCGCAGGAATGGAAGTTCAGGAGTGAAGGC 444

RESULT 4
US-07-945-283-1/c
; Sequence 1, Application US/07945283
; Patent No. 5352596
; GENERAL INFORMATION:
```



APPLICANT: Cheung, Andrew K.  
 APPLICANT: Wesley, Ronald D.  
 TITLE OF INVENTION: Pseudorabies Virus Deletion Mutants  
 TITLE OF INVENTION: Involving The EP0 and LIT Genes  
 NUMBER OF SEQUENCES: 7  
 CORRESPONDENCE ADDRESS:

ADDRESSEE: Curtis P. Ribando  
 STREET: 1815 No. 532596th University Street  
 CITY: Peoria  
 STATE: IL  
 COUNTRY: USA  
 ZIP: 61604

COMPUTER READABLE FORM: disk  
 MEDIUM TYPE: Floppy  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patent In Release #1.0, Version #1.25  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/07/945,283  
 FILING DATE: 19920911  
 CLASSIFICATION: 424

ATTORNEY/AGENT INFORMATION:  
 NAME: Ribando, Curtis P.  
 REGISTRATION NUMBER: 27976  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 309-685-4011 ext.513  
 TELEFAX: 309-685-4128

INFORMATION FOR SEQ ID NO: 1:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 8438 base pairs  
 TYPE: NUCLEIC ACID  
 STRANDEDNESS: double

TOPOLOGY: linear  
 MOLECULE TYPE: DNA (genomic)  
 HYPOTHETICAL: NO  
 ANTI-SENSE: NO  
 ORIGINAL SOURCE:  
 ORGANISM: Pseudorabies virus

FEATURE:  
 NAME/KEY: CDS  
 LOCATION: 622..6495  
 FEATURE:  
 NAME/KEY: variation  
 LOCATION: replace(1099, "g")  
 FEATURE:  
 NAME/KEY: variation  
 LOCATION: replace(1267, "t")  
 FEATURE:  
 NAME/KEY: variation  
 LOCATION: replace(1381, "c")  
 FEATURE:  
 NAME/KEY: variation  
 LOCATION: replace(1566, "c")  
 FEATURE:  
 NAME/KEY: variation  
 LOCATION: replace(7010, "g")  
 US-07-945-283-1

Alignment Scores:  
 Pred. No.: 0.795  
 Score: 90.00  
 Percent Similarity: 40.86%  
 Best Local Similarity: 31.18%  
 Query Match: 14.61%  
 DB: 1

US-09-541-462B-2 (1-108) x US-07-945-283-1 (1-8438)

QY 6 AspValAspThrProSerGlyThrAsnSerGlyAlaGlyLysLysArgPheGluValLys 25  
 Db 1568 GAGTGTAGATGGTCC-----GAGGTCCTGGTGG-TCCCGGGTGGGAGTTAGA 1522  
 QY 26 LysTrpAsnAlaValAlaLeuTrpAlaTrpAspIleValValAspAsnCysAlaIleCys 45

Db 1521 CGATCG-----TGGTCCGTCATG-----GACTGCCCATCTGC 1489  
 QY 46 ArgAsnHisIleMetAspLeuCysIleGluCysGlnAlaAsnGlnAlaSerAlaThrSer 65  
 Db 1488 -----CTGGAGTC-----GCGGCCACC 1471  
 QY 66 GluGluCysThrValAlaLeuTrpGlyValCysAsnHisAlaPheHisCysIleSer 85  
 Db 1470 GAGGCGCAGACGCTGCCG-----TGCATGCACAAAGTTCTGTCTGGACTGCATCCAG 1420  
 QY 86 ArgTrpLeuLysThrArgGlnValCysProLeuAspAsn 98  
 Db 1419 CGCTGGACCTGACGACGACCGCTGCCCGCTGTGCAAT 1381

RESULT 5

US-09-268-140-11  
 ; Sequence 11, Application US/09268140  
 ; Patent No. 6268176  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Gemmill, Robert M.  
 ; APPLICANT: Drabkin, Harry A.  
 ; TITLE OF INVENTION: TRC8 A GENE RELATED TO THE HEDGEHOG RECEPTOR, PATCHED  
 ; FILE REFERENCE: 93445-00004  
 ; CURRENT APPLICATION NUMBER: US/09/268,140  
 ; CURRENT FILING DATE: 2000-03-12  
 ; PRIOR APPLICATION NUMBER: US 60/077,723  
 ; PRIOR FILING DATE: 1998-03-12  
 ; NUMBER OF SEQ ID NOS: 46  
 ; SOFTWARE: Patent In Ver. 2.0  
 ; SEQ ID NO 11  
 ; LENGTH: 2339  
 ; TYPE: DNA  
 ; ORGANISM: Homo sapiens  
 US-09-268-140-11

Alignment Scores:  
 Pred. No.: 0.585  
 Score: 85.00  
 Percent Similarity: 40.48%  
 Best Local Similarity: 28.57%  
 Query Match: 13.80%  
 DB: 3

US-09-541-462B-2 (1-108) x US-09-268-140-11 (1-2339)

QY 20 LysArgPheGluValLysTrpAlaLeuTrpAlaTrpAspIle----- 37  
 Db 1635 CGTAGGACTGCTGAGAGAAATTAATTCACCTCCT-----GAAATAAAGGG 1682  
 QY 38 -----ValValAspAsnCysAlaIleCysArgAsnHisIleMetAspLeu 52  
 Db 1683 AGCCGCTTACAGAAATAAATGATGTATGTGCAATCTGCTATCATGAGTTT----- 1733  
 QY 53 CysIleGluCysGlnAlaAsnGlnAlaSerAlaThrSerGluGluCysThrValAlaTrp 72  
 Db 1734 -----ACAAATCTGCTCGTATTACA----- 1754  
 QY 73 GlyValCysAsnHisAlaPheHisCysIleSerArgTrpLeuLysThrArgGln 92  
 Db 1755 ---CCGTGTAATCATTTATTTCCATGCACCTTCCGTAATGGCTGTACATTCAAGAT 1811  
 QY 93 ValCysProLeu 96  
 Db 1812 ACTTGTCCAATG 1823

RESULT 6

US-09-268-140-11  
 ; Sequence 1, Application US/09268140  
 ; Patent No. 6268176  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Gemmill, Robert M.  
 ; APPLICANT: Drabkin, Harry A.

```
; TITLE OF INVENTION: TRC8, A GENE RELATED TO THE HEDGEHOG RECEPTOR, PATCHED
; FILE REFERENCE: 93445-00004
; CURRENT APPLICATION NUMBER: US/09/268,140
; CURRENT FILING DATE: 2000-03-12
; PRIOR APPLICATION NUMBER: US 60/077,723
; PRIOR FILING DATE: 1998-03-12
; NUMBER OF SEQ ID NOS: 46
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 2505
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (238)..(2232)
US-09-268-140-1
Alignment Scores:
Pred. No.: 0.642 Length: 2505
Score: 85.00 Matches: 24
Percent Similarity: 40.48% Conservative: 10
Best Local Similarity: 28.57% Mismatches: 22
Query Match: 13.80% Indels: 28
DB: 3 Gaps: 4
US-09-541-462B-2 (1-108) x US-09-268-140-1 (1-2505)
QY 20 LysArgPheGluValLysLysTrpAsnAlaValAlaLeuTrpAlaTrpAspLeu 37
Db 1801 CGTAGGACTGCTGTGAAGAAATAATTAATTCACCTCTCT- - - - -GAAATAAAGGG 1848
QY 38 - - - - -ValValAspAsnCysAlaLeuCysArgAsnHisIleMetAspLeu 52
Db 1849 AGCCGCTTACAGAAATAATGATGTGCAATCTGTCATCATGAGTTT- - - - - 1899
QY 53 CysIleGluCysGlnAlaSerAlaThrSerGluGluCysThrValAlaTrp 72
Db 1900 - - - - -ACAACATCTGCTCGTATTACA- - - - - 1920
QY 73 GlyValCysAsnHisAlaPheHisPheHisCysIleSerArgTrpLeuLysThrArgGln 92
Db 1921 - - - - -CCGTGTAATCATATTTCATGCACCTTGCCCTTCGGAATGGCTGTACATTCAAGAT 1977
QY 93 ValCysProLeu 96
Db 1978 ACTTGTCCAATG 1989
RESULT 7
US-09-268-140-7
; Sequence 7, Application US/09268140
; Patent No. 6268176
; GENERAL INFORMATION:
; APPLICANT: Gemmill, Robert M.
; APPLICANT: Drabkin, Harry A.
; TITLE OF INVENTION: TRC8, A GENE RELATED TO THE HEDGEHOG RECEPTOR, PATCHED
; FILE REFERENCE: 93445-00004
; CURRENT APPLICATION NUMBER: US/09/268,140
; CURRENT FILING DATE: 2000-03-12
; PRIOR APPLICATION NUMBER: US 60/077,723
; PRIOR FILING DATE: 1998-03-12
; NUMBER OF SEQ ID NOS: 46
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 7
; LENGTH: 2517
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: repeat unit
; LOCATION: (165)..(176)
US-09-268-140-7
Alignment Scores:
Pred. No.: 0.646 Length: 2517
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Score: 85.00 Matches: 24
Percent Similarity: 40.48% Conservative: 10
Best Local Similarity: 28.57% Mismatches: 22
Query Match: 13.80% Indels: 28
DB: 3 Gaps: 4
US-09-541-462B-2 (1-108) x US-09-268-140-7 (1-2517)
QY 20 LysArgPheGluValLysLysTrpAsnAlaValAlaLeuTrpAlaTrpAspLeu 37
Db 1813 CGTAGGACTGCTGTGAAGAAATAATTAATTCACCTCTCT- - - - -GAAATAAAGGG 1860
QY 38 - - - - -ValValAspAsnCysAlaLeuCysArgAsnHisIleMetAspLeu 52
Db 1861 AGCCGCTTACAGAAATAATGATGTGCAATCTGTCATCATGAGTTT- - - - - 1911
QY 53 CysIleGluCysGlnAlaSerAlaThrSerGluGluCysThrValAlaTrp 72
Db 1912 - - - - -ACAACATCTGCTCGTATTACA- - - - - 1932
QY 73 GlyValCysAsnHisAlaPheHisPheHisCysIleSerArgTrpLeuLysThrArgGln 92
Db 1933 - - - - -CCGTGTAATCATATTTCATGCACCTTGCCCTTCGGAATGGCTGTACATTCAAGAT 1989
QY 93 ValCysProLeu 96
Db 1990 ACTTGTCCAATG 2001
RESULT 8
US-09-325-932A-4
; Sequence 4, Application US/09325932A
; Patent No. 6451604
; GENERAL INFORMATION:
; APPLICANT: Flinn, Barry
; APPLICANT: Lasham, Annette
; TITLE OF INVENTION: Compositions affecting programmed cell
; TITLE OF INVENTION: death and their use in the modification of forestry plant develop
; FILE REFERENCE: 1022
; CURRENT APPLICATION NUMBER: US/09/325,932A
; CURRENT FILING DATE: 1999-06-04
; NUMBER OF SEQ ID NOS: 206
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 4
; LENGTH: 315
; TYPE: DNA
; ORGANISM: Pinus radiata
US-09-325-932A-4
Alignment Scores:
Pred. No.: 0.0674 Length: 315
Score: 83.00 Matches: 17
Percent Similarity: 38.18% Conservative: 4
Best Local Similarity: 30.91% Mismatches: 20
Query Match: 13.47% Indels: 14
DB: 4 Gaps: 1
US-09-541-462B-2 (1-108) x US-09-325-932A-4 (1-315)
QY 42 CysAlaIleCysArgAsnHisIleMetAspLeuCysIleGluCysGlnAlaSerGlnAla 61
Db 74 TCGCGGCTGCTGCTTCCCAAGTTCGAAGACATT- - - - - 106
QY 62 SerAlaThrSerGluGluCysThrValAlaTrpGlyValCysAsnHisAlaPheHisPhe 81
Db 107 - - - - -GAGATTCTCGGTTACTCCCAAGTTCGAGGATCCATTCATCCATC 151
QY 82 HisCysIleSerArgTrpLeuLysThrArgGlnValCysProLeu 96
Db 152 GATTGCATCGATTATTGCTTGAGAGCACTCAAGCTGCCCGCTC 196
RESULT 9
US-08-816-155B-2
; Sequence 2, Application US/08816155B
```

Patent No. 5990091  
GENERAL INFORMATION:  
APPLICANT: TARTAGLIA, JAMES  
APPLICANT: COX, WILLIAM I.  
APPLICANT: GETTIG, RUSSELL R.  
APPLICANT: MARTINEZ, HECTOR  
APPLICANT: PAOLETTI, ENZO  
APPLICANT: PINCUS, STEVEN E.  
TITLE OF INVENTION: VECTORS HAVING ENHANCED EXPRESSION, AND  
METHODS OF MAKING AND USES THEREOF  
NUMBER OF SEQUENCES: 48  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: FROMMER LAWRENCE & HAUG LLP  
STREET: 745 FIFTH AVENUE  
CITY: NEW YORK  
STATE: NEW YORK  
COUNTRY: USA  
ZIP: 10151  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/816,155B  
FILING DATE: 12-MAR-1997  
CLASSIFICATION: 514  
ATTORNEY/AGENT INFORMATION:  
NAME: KOWALSKI, THOMAS J.  
REGISTRATION NUMBER: 32,147  
REFERENCE/DOCKET NUMBER: 454310-2990  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 212-588-0800  
TELEFAX: 212-588-0500  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 4259 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
US-08-816-155B-2

Alignment Scores:  
Pred. No.: 3.64 Length: 4259  
Score: 81.50 Matches: 22  
Percent Similarity: 36.14% Conservative: 8  
Best Local Similarity: 26.51% Mismatches: 22  
Query Match: 13.23% Indels: 31  
DB: 2 Gaps: 4

US-09-541-462B-2 (1-108) x US-08-816-155B-2 (1-4259)

QY	42	CysAlaIleCysArgAsnHisIleMetAspLeuCysIleGluCysGlnAlaAsnGlnAla	61
Db	145	TGTAGCGTATGCTAGAAAGATATACGAAAGAAATAATAAACAA	192
QY	62	SerAlaThrSerGluGluCysThrValAlaTrpGlyVal	78
Db	193	-----TATTTCGGTATTTTACCAAAATGTAACACGCGT	225
QY	79	PheHisPheHisCysIleSerArgTrpLeuLys	92
Db	226	TTTTGTTTCTGTATACACGTTGGATGCTCTATAATAAAGGTACGGATACCGAAGGT	285
QY	93	valCysPro	106
Db	286	ACATGCTCTGTATAGAACAGTTTCTGTTTATATAGTGCTTAATAGTACTGGATAGAC	345
QY	104	GlnLysTyr	106
Db	346	GATAAATAT	354

RESULT 10  
US-09-079-587-2  
Sequence 2, Application US/09079587  
Patent No. 6130066  
GENERAL INFORMATION:  
APPLICANT: TARTAGLIA, JAMES  
APPLICANT: COX, WILLIAM I.  
APPLICANT: GETTIG, RUSSELL R.  
APPLICANT: MARTINEZ, HECTOR  
APPLICANT: PAOLETTI, ENZO  
APPLICANT: PINCUS, STEVEN E.  
TITLE OF INVENTION: VECTORS HAVING ENHANCED EXPRESSION, AND  
METHODS OF MAKING AND USES THEREOF  
NUMBER OF SEQUENCES: 48  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: FROMMER LAWRENCE & HAUG LLP  
STREET: 745 FIFTH AVENUE  
CITY: NEW YORK  
STATE: NEW YORK  
COUNTRY: USA  
ZIP: 10151  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/079,587  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/816,155  
FILING DATE: 12-MAR-1997  
ATTORNEY/AGENT INFORMATION:  
NAME: KOWALSKI, THOMAS J.  
REGISTRATION NUMBER: 32,147  
REFERENCE/DOCKET NUMBER: 454310-2990  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 212-588-0800  
TELEFAX: 212-588-0500  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 4259 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
US-09-079-587-2

Alignment Scores:  
Pred. No.: 3.64 Length: 4259  
Score: 81.50 Matches: 22  
Percent Similarity: 36.14% Conservative: 8  
Best Local Similarity: 26.51% Mismatches: 22  
Query Match: 13.23% Indels: 31  
DB: 3 Gaps: 4

US-09-541-462B-2 (1-108) x US-09-079-587-2 (1-4259)

QY	42	CysAlaIleCysArgAsnHisIleMetAspLeuCysIleGluCysGlnAlaAsnGlnAla	61
Db	145	TGTAGCGTATGCTAGAAAGATATACGAAAGAAATAATAAACAA	192
QY	62	SerAlaThrSerGluGluCysThrValAlaTrpGlyVal	78
Db	193	-----TATTTCGGTATTTTACCAAAATGTAACACGCGT	225
QY	79	PheHisPheHisCysIleSerArgTrpLeuLys	92
Db	226	TTTTGTTTCTGTATACACGTTGGATGCTCTATAATAAAGGTACGGATACCGAAGGT	285
QY	93	valCysPro	106
		-----LeuAspAsnArgGluTrpGluPhe	103







GenCore version 5.1.6  
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OM protein - nucleic search, using frame\_plus\_p2n model

Run on: January 22, 2004, 13:55:35 ; Search time 277 Seconds  
(without alignments)  
1394.436 Million cell updates/sec

Title: US-09-541-462b-2

Perfect score: 616

Sequence: 1 MAAANDVDTPSGTSGAGKK.....KTRQVCLDNREWEFKYGH 108

Scoring table: BLOSUM62

Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 2356869 seqs, 1788235258 residues

Total number of hits satisfying chosen parameters: 4713738

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

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-Q=/cgn2\_1/USPTO.spool/US09541462/runat\_22012004.125830.1585/app.query.fasta\_1.263  
-DB=Published Applications NA -QFMT=fastcap -SUFFIX=rnpb -MINMATCH=0.1  
-LOOPCL=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=BLOSUM62  
-TRANS=human40.cdi -LIST=45 -DOCLALIGN=200 -THR SCORE=pct -THR MAX=100  
-THR MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=ptc -NORM=ext -HEAPSIZ=500 -MINLEN=0  
-MAXLEN=2000000000 -USER=US09541462 @CGN\_1\_1 221 @runat\_22012004.125830.1585  
-NCPUS=6 -ICPU=3 -NO\_MMAP -LARGEQUERY -NSG\_SCORES=0 -WAIT -DSPBLOC=100  
-LONGLOG -DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5  
-FGAPOP=6 -FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Published Applications NA:

- 1: /cgn2\_6/ptodata/1/pubpna/US07\_PUBCOMB.seq\*
- 2: /cgn2\_6/ptodata/1/pubpna/PCT\_NEW\_PUB.seq\*
- 3: /cgn2\_6/ptodata/1/pubpna/US06\_NEW\_PUB.seq\*
- 4: /cgn2\_6/ptodata/1/pubpna/US06\_PUBCOMB.seq\*
- 5: /cgn2\_6/ptodata/1/pubpna/US07\_NEW\_PUB.seq\*
- 6: /cgn2\_6/ptodata/1/pubpna/PCTU5\_PUBCOMB.seq\*
- 7: /cgn2\_6/ptodata/1/pubpna/US08\_NEW\_PUB.seq\*
- 8: /cgn2\_6/ptodata/1/pubpna/US08\_PUBCOMB.seq\*
- 9: /cgn2\_6/ptodata/1/pubpna/US09A\_PUBCOMB.seq\*
- 10: /cgn2\_6/ptodata/1/pubpna/US09B\_PUBCOMB.seq\*
- 11: /cgn2\_6/ptodata/1/pubpna/US09C\_PUBCOMB.seq\*
- 12: /cgn2\_6/ptodata/1/pubpna/US09\_NEW\_PUB.seq\*
- 13: /cgn2\_6/ptodata/1/pubpna/US09\_NEW\_PUB.seq\*
- 14: /cgn2\_6/ptodata/1/pubpna/US10A\_PUBCOMB.seq\*
- 15: /cgn2\_6/ptodata/1/pubpna/US10B\_PUBCOMB.seq\*
- 16: /cgn2\_6/ptodata/1/pubpna/US10\_NEW\_PUB.seq\*
- 17: /cgn2\_6/ptodata/1/pubpna/US60\_NEW\_PUB.seq\*
- 18: /cgn2\_6/ptodata/1/pubpna/US60\_PUBCOMB.seq\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
------------	-------	-------------	--------	----	-------------

ALIGNMENTS

RESULT 1

US-09-918-995-17191  
; Sequence 17191, Application US/09918995  
; Publication No. US20030073623A1  
; GENERAL INFORMATION:  
; APPLICANT: Hyseq, Inc.  
; TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED  
; FILE REFERENCE: 20411-756  
; CURRENT APPLICATION NUMBER: US/09/918,995  
; PRIOR FILING DATE: 2001-07-30  
; PRIOR APPLICATION NUMBER: US/09/235,076  
; PRIOR FILING DATE: 1999-01-20  
; NUMBER OF SEQ ID NOS: 38054  
; SOFTWARE: FastSeq for Windows version 3.0  
; SEQ ID NO 17191  
; LENGTH: 476  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: misc\_feature  
; LOCATION: (1)...(476)  
; OTHER INFORMATION: n = A,T,C or G  
US-09-918-995-17191

Sequence 17191, A  
Sequence 13111, A  
Sequence 4677, Ap  
Sequence 99, Appl  
Sequence 382, App  
Sequence 20, Appl  
Sequence 27, Appl  
Sequence 21, Appl  
Sequence 14771, A  
Sequence 3, Appl1  
Sequence 220, App  
Sequence 38, Appl  
Sequence 498, App  
Sequence 7, Appl1  
Sequence 7, Appl1  
Sequence 7, Appl1  
Sequence 2493, Ap  
Sequence 8547, Ap  
Sequence 8547, Ap  
Sequence 8547, Ap  
Sequence 8547, Ap  
Sequence 27, Appl  
Sequence 732, App  
Sequence 735, App  
Sequence 2188, Ap  
Sequence 14, Appl  
Sequence 487, App  
Sequence 20531, A  
Sequence 38, Appl  
Sequence 222, App  
Sequence 1814, Ap  
Sequence 497, App  
Sequence 19417, A  
Sequence 22557, A  
Sequence 20558, A  
Sequence 751, App  
Sequence 898, App  
Sequence 52, Appl  
Sequence 507, App  
Sequence 1952, Ap  
Sequence 1952, Ap  
Sequence 13085, A  
Sequence 8855, Ap  
Sequence 459, App  
Sequence 21338, A

Alignment Scores:		
Pred. No.:	2,56e-74	Length:
Score:	611.00	Matches:
Percent Similarity:	100.00%	Conservative:
Best Local Similarity:	100.00%	Mismatches:
Query Match:	99.19%	Indels:
DB:	11	Gaps:
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US-09-541-462B-2 (1-108) x US-09-918-995-17191 (1-476)

Qy	2	AlaAlaMetAspValaspThrProSerGlyThrAsnSerGlyAlaGlyLysIysArg	21
Db	75	GCGCAGCGATGTGGATGCCCGAGCGCACCAACAGCGCGCGGCAAGAGCGC	134
Qy	22	PheGluValLysLysTyrAsnAlaValAlaLeuTrpAlaTrpAspIleValValAspAsn	41
Db	135	TTTGAAGTGAANAAGTGGATGCACGTAGCCCTCTGGCGCTGGATATTGTGTTGATAAC	194
Qy	42	CysAlaIleCysArgAsnHisIleMetAspLeuCysIleGluCysGlnAlaAsnGlnAla	61
Db	195	TGTGCCATCTCAGAGAACCATATTATGATCTTTGCATAGAAATGCAAGCTAACCAAGGCG	254
Qy	62	SerAlaThrSerGluGluCysThrValAlaTrpGlyValCysAsnHisAlaPheHisPhe	81
Db	255	TCCGCTACTTCAGAAAGAGTGACTCTGCATGGGGAGTCTGTAAACCATGCTTTTCACTTC	314
Qy	82	HisCysIleSerArgTrpLeuLysThrArgGlnValCysProLeuAspAsnArgGluTrp	101
Db	315	CACTGTCATCTCTCGCTGGCTCAAAACACACAGCAGGTGTGTCCATTGGCAACAGAGATGG	374
Qy	102	GluPheGlnLysTyrGlyHis	108
Db	375	GAATTCCTCAAAAGATATGGGCAC	395

## RESULT 2

```

US-10-198-846-11311/C
; Sequence 11311, Application US/10198846
; Publication No. US2003009974A1
; GENERAL INFORMATION:
; APPLICANT: Lillie, James
; APPLICANT: Xu, Yongyao
; APPLICANT: Wang, Youzhen
; APPLICANT: Steimann, Kathleen
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS
; TITLE OF INVENTION: FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND
; TITLE OF INVENTION: THERAPY OF BREAST CANCER
; FILE REFERENCE: MRI-049
; CURRENT APPLICATION NUMBER: US/10/198,846
; CURRENT FILING DATE: 2002-07-18
; PRIOR APPLICATION NUMBER: 60/306,220
; PRIOR FILING DATE: 2001-07-18
; NUMBER OF SEQ ID NOS: 14084
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 11311
; LENGTH: 4543
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-198-846-11311

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Alignment Scores:	
Pred. No.:	2,169-72
Score:	607.00
Percent Similarity:	100.00%
Best Local Similarity:	100.00%
Query Match:	98.54%
DB:	15
	0
	0
	0
Length:	4543
Matches:	106
Conservative:	0
Mismatches:	0
Indels:	0
Gaps:	0

US-09-541-462B-2 (1-108) x US-10-198-846-11311 (1-4543)

Qy	3	AlaAlaMetAspValAspThrProSerGlyThrAsnSerGlyAlaGlyLysLysArgPhe	22
Db	1085	GCACGGATGGATTGTGGATACCCCGAGCGGCCAACACAGCGCGCGGCAAGAAGCGCTTT	1026

Qy	23	GluValIysLysTrpAsnAlaValAlaLeuTrpAlaTrpAspIleValValAspAsn	Cys 42
Db	1025	GAAGTCAAAAGTGGAAATGCAGTAGCCCTCTGGGCTGGGATATTGTGGTTGATAACTGT	966
Qy	43	AlaIleCysArgAsnHisIleMetAspLeuCysIleGluCysGlnAlaAsnGlnAlaSer	62
Db	965	GCCATCTGCAGGAAACACATTATGGATCTTTGCATAGATGTCAAGCTAACCAAGCGCTCC	906
Qy	63	AlaThrSerGluGluCysThrValAlaTrpGlyValCysAsnHisAlaPheHis	82
Db	905	GCTACTTCAGAGAGTGTACTGTGCGCATGGGAGTCTGTAACCATGCTTTTCACCTCCAC	846
Qy	83	CysIleSerArgTrpLeuIysThrArgGlnValCysProLeuAspAsnArgGluTrpGlu	102
Db	845	TGCATCTCTCGCTGGCTCAAAACACGACAGGTGTGTCATTGGACAAACAGAGATGGGAA	786
Qy	103	PheGlnLysTyrGlyHis 108	
Db	785	TTCCAAAGATATGGGCAC 768	

RESULT 3  
 US-09-960-352-4677  
 ; Sequence 4677, Application US/09960352  
 ; Patent No. US20020137139A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Warren, Wesley C.  
 ; APPLICANT: Tao, Nengbing  
 ; APPLICANT: Wyatt, John C.  
 ; APPLICANT: Mathalagan, Nagapan  
 ; TITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND  
 ; TITLE OF INVENTION: MUSCLE AND FAT DEPOSITION  
 ; FILE REFERENCE: 16511.006/37-21 (10298) C  
 ; CURRENT APPLICATION NUMBER: US/09/960,352  
 ; CURRENT FILING DATE: 2001-09-24  
 ; NUMBER OF SEQ ID NOS: 15112  
 ; SEQ ID NO 4677  
 ; LENGTH: 380  
 ; TYPE: DNA  
 ; ORGANISM: Bos taurus  
 ; OTHER INFORMATION: Clone ID: 20-LIB34-034-Q1-E1-E7  
 US-09-960-352-4677

Alignment Scores:	
Pred. No.:	2,158-72
Score:	536.00
Percent Similarity:	100.00%
Best Local Similarity:	98.10%
Query Match:	96.75%
DB:	10
	Length:
	Matches:
	Conservative:
	Mismatches:
	Indels:
	Gaps:
	380
	103
	2
	0
	0
	0

US-09-541-462B-2 (1-108) x US-09-960-352-4677 (1-380)

Qy	4	AlaMetAspValAspThrProSerGlyThrAsnSerGlyAlaGlyLysLysAspGlu	23
Db	4	GCGATGGATGTGGATACCCAGCGCGCACCAACACAGCGCGCGCAAGAGCGCTTTGAA	63
Qy	24	ValLysLysTrpAsnAlaValAlaLeuTrpAlaTrpAspIleValValAspAsnCysAla	43
Db	64	GTGMAAAGTGGAAATGCGAGTAGCCCTCTGGGCCCTGGGATATTGTGGTTGATACTGTGCC	123
Qy	44	IleCysArgAsnHisIleMetAspLeuCysIleGluCysGlnAlaAsnGlnAlaSerAla	63
Db	124	ATCTGCAGGAACCAATATTATGGATCTTTTGGCATAGAAATGTCAGAGCAACACGAGCGTCGCCT	183
Qy	64	ThrSerGluGluCysThrValAlaTrpGlyValCysAsnHisAlaPheHisPheHisCys	83
Db	184	ACTCTGAAGATGCACCGTGCCTGGGGGCGCTGTAAACCATGCTTTTCACTTCCACTGC	243
Qy	84	IleSerArgTrpLeuLysThrArgGlnValCysProLeuAspAsnAArgLysTrpGluPhe	103
Db	244	ATCTCTCGTGTGCTCAAAACACACAGAGGTGTGCTCGTTGGACACACAGAGATGGGAATTC	303



QY 104 GlnLysTyrGlyHis 108  
|||:|||||  
Db 304 CAAAGTATGGGCAC 318

## RESULT 4

US-10-240-965-99/c  
; Sequence 99, Application US/10240965  
; Publication No. US20030165924A1  
; GENERAL INFORMATION:  
; APPLICANT: INCYTE GENOMICS, INC.  
; APPLICANT: SHIFMAN, Dov  
; APPLICANT: SOMOGYI, Roland  
; APPLICANT: LAWN, Richard M.  
; APPLICANT: SEILHAMER, Jeffrey J.  
; APPLICANT: PORTER, Gordon J.  
; APPLICANT: MIKITA, Thomas  
; APPLICANT: TAI, Julie  
; TITLE OF INVENTION: GENES EXPRESSED IN FOAM CELL DIFFERENTIATION  
; FILE REFERENCE: PA-0025 PCT  
; CURRENT APPLICATION NUMBER: US/10/240,965  
; CURRENT FILING DATE: 2002-10-04  
; PRIOR APPLICATION NUMBER: 60/195,106  
; PRIOR FILING DATE: 2000-04-05  
; NUMBER OF SEQ ID NOS: 276  
; SOFTWARE: PERL Program  
; SEQ ID NO 99  
; LENGTH: 5347  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: misc feature  
; OTHER INFORMATION: Incyte ID No. US20030165924A1 364940.19  
US-10-240-965-99

## Alignment Scores:

Pred. No.: 1,276-67 Length: 5347  
Score: 573.00 Matches: 103  
Percent Similarity: 99.04% Conservative: 0  
Best Local Similarity: 99.04% Mismatches: 0  
Query Match: 93.02% Indels: 1  
DB: 13 Gaps: 0

US-09-541-462B-2 (1-108) x US-10-240-965-99 (1-5347)

QY 3 AlaAlaMetAspValAspThrProSerGlyThrAsnSerGlyVala-GlyLysLysArgPh 22  
|||:|||||  
Db 515 GCAGCGATGGATGTGGATACCCCGAGCGGCCCAACAGCGCGCGCGGCAAGAGCGCTT 456  
|||:|||||  
QY 22 eGluValLysLysTrpAsnAlaValAlaLeuTrpAlaTrpAspIleValValAspAsnCy 42  
|||:|||||  
Db 455 TGAAGTGAAAAAGTGAATGCAGTACCCCTCTGGGCTGGGATATTGTGGTTGATAACTG 396  
|||:|||||  
QY 42 salalleCysArgAsnHisIleMetAspLeuCysIleGluCysGlnAlaAsnGlnAlase 62  
|||:|||||  
Db 395 TGCCATCTCGAGAACCCACATTATGGATCTTTGCATAGAATGTCAAGCTAACCCAGCGTC 336  
|||:|||||  
QY 62 rAlaThrSerGluGluCysThrValalatrpglyValCysAsnHisAlaPheHis 82  
|||:|||||  
Db 335 CGTACTCTCAGAAAGTGTACTCTCGCATGGGGAGTCTGTAAACCATGCTTTTCACCTCCA 276  
|||:|||||  
QY 82 sCysIleSerArgTrpLeuLysThrArgGlnValCysProLeuAspAsnArgGluTrpG1 102  
|||:|||||  
Db 275 CTGCACTCTCGTGGCTCAAAACACAGCAGAGGTGTGTCTCCATTGGACACAGAGATGGGA 216  
|||:|||||  
QY 102 uPheGlnLys 105  
|||:|||||  
Db 215 ATTCCAAAAG 206  
|||:|||||

## RESULT 5

US-10-205-823-382/c  
; Sequence 382, Application US/10205823  
; Publication No. US20030108963A1  
; GENERAL INFORMATION:

; APPLICANT: Schlegel, Robert  
; APPLICANT: Monahan, John E.  
; APPLICANT: Endege, Wilson O.  
; APPLICANT: Gannavarapu, Manjula  
; APPLICANT: Gorbacheva, Bella  
; APPLICANT: Hoersch, Sebastian  
; APPLICANT: Kamatkar, Shubhangi  
; APPLICANT: Wansley, Angela M.  
; APPLICANT: Glatt, Karen  
; APPLICANT: Zhao, Xumei  
; APPLICANT: Anderson, Dustin  
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND  
; TITLE OF INVENTION: METHODS FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND  
; FILE REFERENCE: MRI-044  
; CURRENT APPLICATION NUMBER: US/10/205,823  
; CURRENT FILING DATE: 2002-07-25  
; PRIOR APPLICATION NUMBER: 60/307,982  
; PRIOR FILING DATE: 2001-07-25  
; PRIOR APPLICATION NUMBER: 60/314,356  
; PRIOR FILING DATE: 2001-08-22  
; PRIOR APPLICATION NUMBER: 60/325,020  
; PRIOR FILING DATE: 2001-09-25  
; PRIOR APPLICATION NUMBER: 60/341,746  
; PRIOR FILING DATE: 2001-12-12  
; PRIOR APPLICATION NUMBER: 60/362,158  
; PRIOR FILING DATE: 2002-03-05  
; NUMBER OF SEQ ID NOS: 455  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 382  
; LENGTH: 5111  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-205-823-382

Alignment Scores:  
Pred. No.: 4,856-65 Length: 5111  
Score: 554.00 Matches: 98  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 89.94% Indels: 0  
DB: 15 Gaps: 0

US-09-541-462B-2 (1-108) x US-10-205-823-382 (1-5111)

QY 3 AlaAlaMetAspValAspThrProSerGlyThrAsnSerGlyValaGlyLysLysArgPhe 22  
|||:|||||  
Db 296 GCAGCGATGGATGTGGATACCCCGAGCGGCCCAACAGCGCGCGCGGCAAGAGCGCTT 237  
|||:|||||  
QY 23 GluValLysLysTrpAsnAlaValAlaLeuTrpAlaTrpAspIleValValAspAsnCy 42  
|||:|||||  
Db 236 GAAGTGAAAAAGTGAATGCAGTACCCCTCTGGGCTGGGATATTGTGGTTGATAACTGT 177  
|||:|||||  
QY 43 AlalleCysArgAsnHisIleMetAspLeuCysIleGluCysGlnAlaAsnGlnAlaSer 62  
|||:|||||  
Db 176 GCCATCTCGAGAACCCACATTATGGATCTTTGCATAGAATGTCAAGCTAACCCAGCGTCC 117  
|||:|||||  
QY 63 AlaThrSerGluGluCysThrValalatrpglyValCysAsnHisAlaPheHis 82  
|||:|||||  
Db 116 GCTACTCTCAGAAAGTGTACTCTCGCATGGGGAGTCTGTAAACCATGCTTTTCACITCCAC 57  
|||:|||||  
QY 83 CysIleSerArgTrpLeuLysThrArgGlnValCysProLeuAspAsnArgGlu 100  
|||:|||||  
Db 56 TGCATCTCTCGTGGCTCAAAACACAGCAGAGGTGTGTCTCCATTGGACACAGAGAG 3  
|||:|||||

## RESULT 6

US-09-770-791-20  
; Sequence 20, Application US/09770791  
; Patent No. US20020062014A1  
; GENERAL INFORMATION:  
; APPLICANT: Gorlach, Jörn  
; APPLICANT: An, Yong-Qiang  
; APPLICANT: Hamilton, Carol M.



```
/ LENGTH: 3208
/ TYPE: DNA
/ ORGANISM: homo sapiens
US-10-214-811-27

Alignment Scores:
Pred. No.: 4,09e-58 Length: 3208
Score: 501.50 Matches: 88
Percent Similarity: 95.70% Conservative: 1
Best Local Similarity: 94.62% Mismatches: 1
Query Match: 81.41% Indels: 3
DB: 15 Gaps: 1

US-09-541-462B-2 (1-108) x US-10-214-811-27 (1-3208)

QY 16 GlyAlaGlyLysArgPheGluValLysTyrAsnAlaValAlaLeuTrpAlaTrp 35
DB 2752 GGAGCATAAATAAAAAA-----AAAATAAGTAAGCAGTACCCCTCTGGGCTGG 2802

QY 36 AspIleValAlaAspAsnCysAlaIleCysArgAsnHisIleMetAspLeuCysIleGlu 55
DB 2803 GATATTGTGGTTGATAAATCGCATCTGCAGGAACACATTATGATCTTTGCATAGAA 2862

QY 56 CysGlnAlaAsnGlnAlaSerAlaThrSerGluGluCysThrValAlaTrpGlyValCys 75
DB 2863 TGTCAAGCTAAACACAGCGCTCGCTACTTCAGAAAGAGTGTACTGCGCATGGGAGTCTGT 2922

QY 76 AsnHisAlaPheHisPheHisCysIleSerArgTyrLeuLysThrArgGlnValCysPro 95
DB 2923 AACCATGCTTTTCACTTCACATCGATCTCTCGCTGGCTCAAAACACGACGAGTGTGCCA 2982

QY 96 LeuAspAsnArgGluTrpGluPheGlnLysTyrGlyHis 108
DB 2983 TTGGACAACACAGAGTGGGAATTCGAAAGATATGGGCAC 3021

RESULT 9
US-09-918-995-14771
; Sequence 14771, Application US/09918995
; Publication No. US20030073623A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc.
; TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
; FILE REFERENCE: FROM VARIOUS CDNA LIBRARIES
; CURRENT FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: US/09/918,995
; PRIOR FILING DATE: 2001-07-30
; NUMBER OF SEQ ID NOS: 38054
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 14771
; LENGTH: 439
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-918-995-14771

Alignment Scores:
Pred. No.: 7,74e-45 Length: 439
Score: 396.00 Matches: 67
Percent Similarity: 98.55% Conservative: 1
Best Local Similarity: 97.10% Mismatches: 1
Query Match: 64.29% Indels: 0
DB: 11 Gaps: 0

US-09-541-462B-2 (1-108) x US-09-918-995-14771 (1-439)

QY 27 TrpAsnAlaValAlaLeuTrpAlaTrpAspIleValAlaAspAsnCysAlaIleCysArg 46
DB 232 TGGATGACGATATCCCTCTGGGCTGGGATATTGTGGATTAATGTCATCTGCAGG 291

QY 47 AsnHisIleMetAspLeuCysIleGluCysGlnAlaAsnGlnAlaSerAlaThrSerGlu 66
DB 292 AACCATATTATGATCTTTTGCATAGAAATGTCAAGCTAACACAGCGCTCCGCTACTTCAGAA 351
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QY 67 GluCysThrValAlaTrpGlyValCysAsnHisAlaPheHisPheHisCysIleSerArg 86
DB 352 GAGTGTACTGTGCGCATGGGAGTCTGTAAACCATGCTTTTCACTTCACATGCTCTCGC 411

QY 87 TrpLeuLysThrArgGlnValCysPro 95
DB 412 TGGCTCAAAACACGACGAGTGTGTCCA 438

RESULT 10
US-10-017-721-3
; Sequence 3, Application US/10017721
; Publication No. US20030096248A1
; GENERAL INFORMATION:
; APPLICANT: McCarthy, Jeanette
; APPLICANT: Bolk, Stacey
; TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF VASCULAR DISEASE
; FILE REFERENCE: MMI-003
; CURRENT APPLICATION NUMBER: US/10/017,721
; PRIOR FILING DATE: 2001-12-14
; PRIOR APPLICATION NUMBER: US 60/317,033
; PRIOR FILING DATE: 2001-09-04
; PRIOR APPLICATION NUMBER: US 60/330,248
; PRIOR FILING DATE: 2001-10-17
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 175561
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-017-721-3

Alignment Scores:
Pred. No.: 3,29e-35 Length: 175561
Score: 352.50 Matches: 75
Percent Similarity: 78.70% Conservative: 10
Best Local Similarity: 69.44% Mismatches: 20
Query Match: 57.22% Indels: 5
DB: 15 Gaps: 1

US-09-541-462B-2 (1-108) x US-10-017-721-3 (1-175561)

QY 1 MetAlaAlaAlaMetAspValAspThrProSerGlyThrAsnSerGlyAlaGlyLysLys 20
DB 59458 ATGGCAGTGGCAATGGATGTGGATACCCCAAGAAGTACCAACAGCAGTCTTTGAAGTAA 59517

QY 21 ArgPheGluValLysLysTrpAsnAlaValAlaLeuTrpAlaTrpAspIleValAlaAsp 40
DB 59518 AAAAGTGAATGCAG-----TAGCTAGCCCTCTGGGCTTGGGATGTTTGTGTTAAT 59568

QY 41 AsnCysAlaIleCysArgAsnHisIleMetAspLeuCysIleGluCysGlnAlaAsnGln 60
DB 59569 AACTGTGCCATCTGCAGGAATCAGCATGATC--TGCATTGAATGTCAAGCTAACCAA 59626

QY 61 AlaSerAlaThrSerGluGluCysThrValAlaTrpGlyValCysAsnHisAlaPheHis 80
DB 59627 GAGTCTGCCATCTCAGAACTGTGTACCGTTGCACGGGAGCCCTGTAAACCGTCTTTTCAC 59686

QY 81 PheHisCysIleSerArgTrpLeuLysThrArgGlnValCysProLeuAspAsnArgGlu 100
DB 59687 TT-CACTGTCTCTCACTGGCTCAAAACACAAACAGCTGTGCTGCTGTTGGACAACAGCAA 59745

QY 101 TrpGluPheGlnLysTyrGlyHis 108
DB 59746 TAGGAATCCCAAGATATGGACAC 59769

RESULT 11
US-09-962-436-220/C
; Sequence 220, Application US/09962436
; Patent No. US20020081301A1
; GENERAL INFORMATION:
; APPLICANT: Soppet, Daniel
```

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; TITLE OF INVENTION: Cancer Gene Determination and Therapeutic Screening Using Signat
; TITLE OF INVENTION: Sets
; FILE REFERENCE: 689290-75
; CURRENT APPLICATION NUMBER: US/09/962,436
; CURRENT FILING DATE: 2001-09-25
; PRIOR APPLICATION NUMBER: US/60/235,082
; PRIOR FILING DATE: 2000-09-25
; PRIOR APPLICATION NUMBER: US/60/234,924
; PRIOR FILING DATE: 2000-09-25
; NUMBER OF SEQ ID NOS: 568
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 220
; LENGTH: 418
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-962-436-220

Alignment Scores:
Pred. No.: 139e-30 Length: 418
Score: 292.00 Matches: 58
Percent Similarity: 84.42% Conservative: 7
Best Local Similarity: 75.32% Mismatches: 12
Query Match: 47.40% Indels: 2
DB: 9 Gaps: 0

US-09-541-462B-2 (1-108) x US-09-962-436-220 (1-418)
QY 32 LeuTrpAlaTrpAspIleValValAspAsnCyAlaIleCysArgAsnHisIleMetAsp 51
Db 418 GTCTGGCGCTGGGATGTTGGTAACTGTGCCATCTGCAGGAATCACGATGGAT 359
QY 52 LeuCysIleGluCysGlnAlaAsnGlnAlaSerAlaThrSerGluGluCysThrValAla 71
Db 358 C--TGCATTGAATGTCAGCTAACCAAGAGCTCTGCCACITTCAGAAGTGTGTCACGTTGCA 301
QY 72 TrpGlyValCysAsnHisAlaPheHisPheHisCysIleSerArgTrpLeuLysThrArg 91
Db 300 CGGGAGCGCTGTAAACCGTGTCTTTTCATT--CACTGTCTCTCTCAGTGGCTCAAAACACAA 242
QY 92 GlnValCysProLeuAspAsnArgGluTrpGluPheGlnLysTyrGlyHis 108
Db 241 CAGCTGTGCTGTGTGGCAACACAGACAATAGGAATTCCTCAAGATGGACAC 191

RESULT 12
US-09-764-864-39
; Sequence 39 Application US/09764864
; Patent No. US20020132753A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PT23
; CURRENT APPLICATION NUMBER: US/09/764,864
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 1792
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 39
; LENGTH: 836
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-764-864-39

Alignment Scores:
Pred. No.: 3.68e-30 Length: 836
Score: 292.00 Matches: 49
Percent Similarity: 64.95% Conservative: 14
Best Local Similarity: 50.52% Mismatches: 30
Query Match: 47.40% Indels: 4
DB: 10 Gaps: 2

US-09-541-462B-2 (1-108) x US-09-764-864-39 (1-836)
QY 11 SerGlyThrAsnSerGlyAlaGlyLysLysArgPheGluValLysLysTrpAsnAlaVal 30

```

US-09-826-312-7  
; Sequence 7, Application US/09826312  
; Patent No. US20020042083A1  
; GENERAL INFORMATION:  
; APPLICANT: Iseakani, Sarkiz D.  
; APPLICANT: Huang, Jianing  
; APPLICANT: Sheung, Julie  
; APPLICANT: Pray, Todd R.  
; TITLE OF INVENTION: UBIQUITIN LIGASE ASSAY  
; FILE REFERENCE: A-68613-1/RMS/JJD  
; CURRENT APPLICATION NUMBER: US/09/826,312  
; CURRENT FILING DATE: 2001-04-03  
; PRIOR APPLICATION NUMBER: US 09/542,497  
; PRIOR FILING DATE: 2000-04-03  
; NUMBER OF SEQ ID NOS: 17  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 7

; LENGTH: 342  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-826-312-7

Alignment Scores:  
Pred. No.: 5,09e-30 Length: 342  
Score: 287.00 Matches: 48  
Percent Similarity: 63.92% Conservative: 14  
Best Local Similarity: 49.48% Mismatches: 31  
Query Match: 46.59% Indels: 4  
DB: 9 Gaps: 2

US-09-541-462B-2 (1-108) x US-09-826-312-7 (1-342)

```
QY 11 SerGlyThrAsnSerGlyAlaGlyLysLysArgPheGluValLysLysTrpAsnAlaVal 30
   |||||...|||...|||...|||...|||...|||...|||...|||...|||...|||...|||
Db 58 TCAGGCTCAACGTCGGGA---GGCGACAAGATGTTCTCCCTCAAGAAGTGGAAACCGGTG 114
   |||||...|||...|||...|||...|||...|||...|||...|||...|||...|||
QY 31 AlaLeuTrpAlaTrpAspIleValValAspAsnCysAlaIleCysArgAsnHisIleMet 50
   |||||...|||...|||...|||...|||...|||...|||...|||...|||...|||
Db 115 GCCATGTGAGCTGGGACGTGGAGTACGTACGTGCGCCATCTGCAGGTCCAGGTGATG 174
   |||||...|||...|||...|||...|||...|||...|||...|||...|||...|||
QY 51 AspLeuCysIleGluCysGlnAlaAsnGlnAlaSerAlaThrSerGluGluCysThrVal 70
   |||||...|||...|||...|||...|||...|||...|||...|||...|||...|||
Db 175 GATGCTGTCTTAGATGTCAAGCTGAAAC-----AAACAAGAGGACTGTGTTGTG 225
   |||||...|||...|||...|||...|||...|||...|||...|||...|||...|||
QY 71 AlaTrpGlyValCysAsnHisAlaPheHisPheHisCysIleSerArgTrpLeuLysThr 90
   |||||...|||...|||...|||...|||...|||...|||...|||...|||...|||
Db 226 GTCTGGGGAGATGTAATCATTCCTTCCACAACACTGCTGCATGCTCCCTGGGTGAAACAG 285
   |||||...|||...|||...|||...|||...|||...|||...|||...|||...|||
QY 91 ArgGlnValCysProLeuAspAsnArgGluTrpGluPheGlnLysTyrGly 107
   |||||...|||...|||...|||...|||...|||...|||...|||...|||...|||
Db 286 AACAAATCGTGCCTCTCTGCCAGCAGGACTGGGTGGTCCCAAGAATCGGC 336
   |||||...|||...|||...|||...|||...|||...|||...|||...|||...|||
```

RESULT 15

US-10-108-767-7

; Sequence 7, Application US/10108767  
; Publication No. US2003010474A1  
; GENERAL INFORMATION:  
; APPLICANT: Iseakani, Sarkiz D.  
; APPLICANT: Huang, Jianing  
; APPLICANT: Sheung, Julie  
; APPLICANT: Pray, Todd R.  
; TITLE OF INVENTION: ASSAYS FOR IDENTIFYING UBIQUITIN AGENTS AND FOR IDENTIFYING AGENT  
; FILE REFERENCE: A-68613-5/RMS/DCF  
; CURRENT APPLICATION NUMBER: US/10/108,767  
; CURRENT FILING DATE: 2002-09-26  
; PRIOR APPLICATION NUMBER: US 09/542,497  
; PRIOR FILING DATE: 2000-04-03  
; PRIOR APPLICATION NUMBER: US 09/826,312  
; PRIOR FILING DATE: 2001-04-03  
; PRIOR APPLICATION NUMBER: US 10/091,139  
; PRIOR FILING DATE: 2002-03-04  
; NUMBER OF SEQ ID NOS: 27

; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 7  
; LENGTH: 342  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-108-767-7

Alignment Scores:  
Pred. No.: 5,09e-30 Length: 342  
Score: 287.00 Matches: 48  
Percent Similarity: 63.92% Conservative: 14  
Best Local Similarity: 49.48% Mismatches: 31  
Query Match: 46.59% Indels: 4  
DB: 15 Gaps: 2

US-09-541-462B-2 (1-108) x US-10-108-767-7 (1-342)

```
QY 11 SerGlyThrAsnSerGlyAlaGlyLysLysArgPheGluValLysLysTrpAsnAlaVal 30
   |||||...|||...|||...|||...|||...|||...|||...|||...|||...|||
Db 58 TCAGGCTCAACGTCGGGA---GGCGACAAGATGTTCTCCCTCAAGAAGTGGAAACCGGTG 114
   |||||...|||...|||...|||...|||...|||...|||...|||...|||...|||
QY 31 AlaLeuTrpAlaTrpAspIleValValAspAsnCysAlaIleCysArgAsnHisIleMet 50
   |||||...|||...|||...|||...|||...|||...|||...|||...|||...|||
Db 115 GCCATGTGAGCTGGGACGTGGAGTACGTACGTGCGCCATCTGCAGGTCCAGGTGATG 174
   |||||...|||...|||...|||...|||...|||...|||...|||...|||...|||
QY 51 AspLeuCysIleGluCysGlnAlaAsnGlnAlaSerAlaThrSerGluGluCysThrVal 70
   |||||...|||...|||...|||...|||...|||...|||...|||...|||...|||
Db 175 GATGCTGTCTTAGATGTCAAGCTGAAAC-----AAACAAGAGGACTGTGTTGTG 225
   |||||...|||...|||...|||...|||...|||...|||...|||...|||...|||
QY 71 AlaTrpGlyValCysAsnHisAlaPheHisPheHisCysIleSerArgTrpLeuLysThr 90
   |||||...|||...|||...|||...|||...|||...|||...|||...|||...|||
Db 226 GTCTGGGGAGATGTAATCATTCCTTCCACAACACTGCTGCATGCTCCCTGGGTGAAACAG 285
   |||||...|||...|||...|||...|||...|||...|||...|||...|||...|||
QY 91 ArgGlnValCysProLeuAspAsnArgGluTrpGluPheGlnLysTyrGly 107
   |||||...|||...|||...|||...|||...|||...|||...|||...|||...|||
Db 286 AACAAATCGTGCCTCTCTGCCAGCAGGACTGGGTGGTCCCAAGAATCGGC 336
   |||||...|||...|||...|||...|||...|||...|||...|||...|||...|||
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Job time : 294 secs

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